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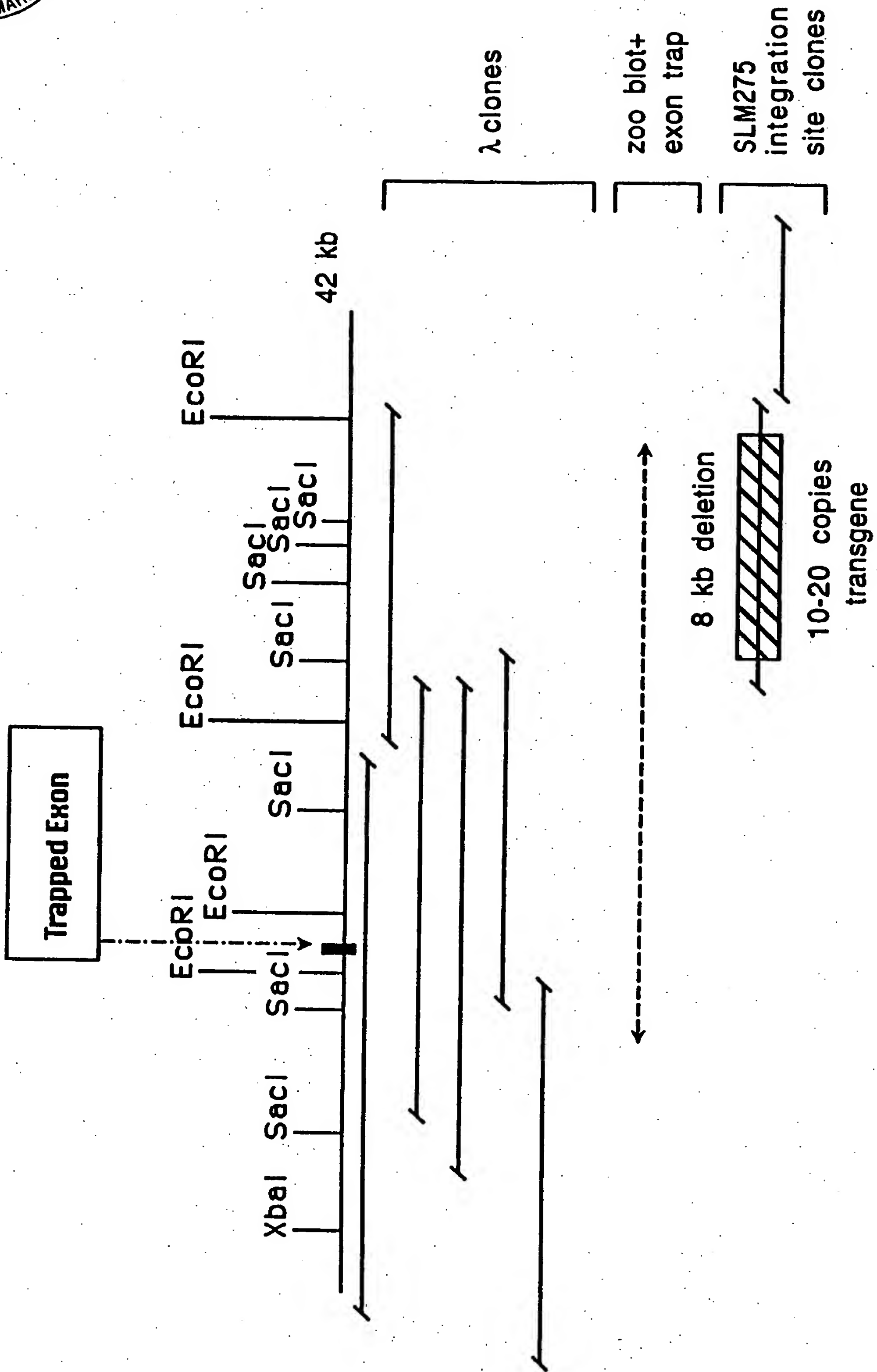


FIG.1



SEQ ID NO:1 m-del1	DL	LLVPTKVTG	IITQG--AKD	FGDVLFGVGSY	KLAYSNDGEH	WMVHQDEKQR	cont.
SEQ ID NO:2 h-MFG	DL	GSSKEVTG	IITQG--ARN	FGSVQFVASV	KVAYSNDSAN	WTEYQDPRTG	cont.
SEQ ID NO:3 h-FV	DL	LKIKKITA	IITQG--CKS	LSSEMYVKSY	TIHYSEQGVE	WKPYRLKSSM	cont.
SEQ ID NO:4 m-FV111	DL	QKTMKVTG	IITQG--VKS	LFTSMFVKEF	LISSSQDGH	WT--QILYNG	cont.
SEQ ID NO:5 X-A5b1	DL	ENLRFVSG	IGTQGAISKE	TKKKYFVKSY	KVDISSNGED	WI-TLKDGN	cont.
SEQ ID NO:6 X-A5b2	DL	AEEKIVRG	VITQG--GKH	KENKVFMRKF	KIGYSNNGTE	WEMIMDSSKN	cont.
SEQ ID NO:7 dis-1	G	CEVPRTFMC	VALQC---RG	-DADQWVTSY	KIRYSLDNVS	WF-----EYR	cont.
SEQ ID NO:8 CONSENSUS	DL	.....VTG	IITQG--K.	.....FV.SY	KI.YS.DG..	W.....	cont.

SEQ ID NO:1 m-del1	KDKVFQGNFD	NDTHRKNVID	PPIYARFIRI	LPL--
SEQ ID NO:2 h-MFG	SSKVFQGNLD	NNSHKKNI	FE	KPFMARVVRV
SEQ ID NO:3 h-FV	VDKIFE	GNTN	TKGHVKNFFN	PPIISRFIRV
SEQ ID NO:4 m-FV111	KVKVFQGNQD	SSTPMMNSLD	PPLLTR----	
SEQ ID NO:5 X-A5b1	KHLVFTGNTD	ATDVVYRPFS	KPVI	TRFVRL
SEQ ID NO:6 X-A5b2	KPKTFEGNTN	YDTPELRTF-	AHIT	TGFIRI
SEQ ID NO:7 dis-1	NGAAITGVTD	RNTVVNHFFD	TPIRAR	SI
SEQ ID NO:8 CONSENSUS	K.KVF.GNTD	..T....N.F.	.PI..RFIR.	.P.

FIG. 2

EcoRI HpaI

GAATTCCGGT TAACTGAGGA CAAAGGGTAA TGCAGAAGTG ATATTGATT TCCATTCTCA 60

DraI

TCCCAGTGG CCTTGATATT TAACTGATT CCTGCCACCA GGTCTTGGG CCACCCTGTC 120

EspBI SphI

CCTGCGTCTC ATATTTCGCG ATGCTGCTTT GTTTGTATAT AGTGGCTCC TGGCCTCAGG 180

CTCGCTCCCC TCCAGCTCTC GCTTCATTGT TCTCCAAGTC AGAAGCCCCC GCATCCGCCC 240

BssHII

CGCAGCAGCG TGAGCCGTAG TCACTGCTGG CCGCTTCGCC TGGCTGCGCG CACGGAAATC 300

GGGAGCCAG GAACCCAAGG AGCCGCCGTC CGCCCGCTGT GCCTCTGCTA GACCACTCGC 360

AGCCCCAGCC TCTCTCAAGC GCACCCACCT CCGCGCACCC CAGCTCAGGC GAAGCTGGAG 420

TGAGGGTGAA TCACCCTTTC TCTAGGCCCA CCACTCTTTT ATCGCCCTTC CCAAGATTTC 480

Eco47III AatII

AGAAGCGCTG CGGAGGAAA GACGTCCTCT TGATCTCTGA CAGGGCGGGG TTTACTGCTG 540

BssHIII PstI

TCCTGCAGGC GCGCCTCGCC TACTGTGCCC TCCGCTACGA CCCCAGGACCA GCCCAGGTCA 600

BspHI

CGTCCGTGAG AAGGGATCAT GAAGCACTTG GTAGCAGCCT GGCTTTTGGT TGGACTCAGC 660

M K H L V A A W L L V G L S

CTCGGGGTGC CCCAGTTCGG CAAAGGTGAC ATTTGCAACC CGAACCCCTG TGAAAATGGT 720

L G V P Q F G K G D I C N P N P C E N G

FIG. 3A



BspMI  
GGCATCTGTC TGTCAGGACT GGCTGATGAT TCCTTTTCCT GTGAGTGTCC AGAAGGCTTC 780  
G I C L S G L A D D S F S C E C P E G F

BspMI  
GCAGGTCCGA ACTGCTCTAG TGTGTGGAG GTTGCATCAG ATGAAGAAAA GCCTACTTCA 840  
A G P N C S S V V E V A S D E E K P T S

GCAGTCCCT GCATCCCTAA CCCATGCCAT AACGGAGGAA CCTGTGAGAT AAGCGAAGCC 900  
A G P C I P N P C H N G G T C E I S E A

TATCGAGGAG ACACATTCAT AGGCTATGTT TGTAATGTC CTCGGGGATT TAATGGGATT 960  
Y R G D T F I G Y V C K C P R G F N G I

CACTGTCAGC ACAATATAAA TGAATGTGAA GCTGAGCCTT GCAGAAATGG CGGAATATGT 1020  
H C Q H N I N E C E A E P C R N G G I C

BsmI  
ACCGACCTTG TTGCTAACTA CTCTTGTAAG TGCCAGGAG AATTATGGG ACGAAATTGT 1080  
T D L V A N Y S C E C P G E F M G R N C

CAATATAAAT GCTCTGGGCA CTTGGGAATC GAAGGTGGGA TCATATCTAA TCAGCAAATC 1140  
Q Y K C S G H L G I E G G I I S N Q Q I

SacI  
Ec1136II  
ACAGCTTCAT CTAATCACCG AGCTCTTTT GGAAGTCCAGA AGTGGTATCC CTACTATGCT 1200  
T A S S N H R A L F G L Q K W Y P Y Y A

NcoI  
MscI  
BclI  
PvuII  
CGACTTAATA AGAAGGGCCT TATAAATGCC TGGACAGCTG CTGAAAATGA CAGATGGCCA 1260  
R L N K K G L I N A W T A A E N D R W P

TGGATTCAGA TAAATTGCA AAGAAAAATG AGAGTCACTG GTGTTATTAC CCAAGGAGCA 1320  
W I Q I N L Q R K M R V T G V I T Q G A

AAAAGGATTG GAAGCCCAGA GTACATAAAA TCCTACAAAA TTGCCTACAG CAATGACGGG 1380  
K R I G S P E Y I K S Y K I A Y S N D G

FIG.3B



09/237,981  
AU: 1644

BbsI EorI  
AAGACCTGGG CAATGTACAA AGTAAAAGGC ACCAATGAAG AGATGGTCTT TCGTGAAAT 1440  
K T W A M Y K V K G T N E E M V F R G N

NdeI  
GTTGATAACA ACACACCATA TGCTAATTCT TTCACACCCC CAATCAAAGC TCAGTATGTA 1500  
V D N N T P Y A N S F T P P I K A Q Y V

AGACTCTACC CCCAAATTG TCGAAGGCAT TGTACTTTAA GAATGGAAC TCTTGGCTGT 1560  
R L Y P Q I C R R H C T L R M E L L G C

SacI  
Ecl136II  
GAGCTCTCAG GCTGTTTACA ACCTTTGGGG ATGAAATCAG GGCATATACA AGACTACCAG 1620  
E L S G C S E P L G M K S G H I Q D Y Q

BbsI  
ATCACTGCCT CCAGCGTCTT CAGAACAATC AACATGGACA TGTTTACTTG GGAACCAAGG 1680  
I T A S S V F R T L N M D M F T W E P R

AAAGCCAGGC TGGACAAGCA AGGCAAAGTA AATGCCTGGA CTTCCGGCCA TAACGACCAG 1740  
K A R L D K Q G K V N A W T S G H N D Q

TCACAATGGT TACAGGTGTA TCTTCTTGTC CCTACTAAGG TGACAGGCAT CATTACACAA 1800  
S Q W L Q V D L L V P T K V T G I I T Q

PmlI  
GGAGCTAAAG ATTTTGGTCA CGTGCAGTTT GTTGGGTCAT ACAAACACTAGC TTACAGCAAT 1860  
G A K D F G H V Q F V G S Y K L A Y S N

ApoLI  
GATGGAGAAC ACTGGATGGT GCACCAGGAT GAAAAACAGA GGAAAGACAA GGTTTTTCAA 1920  
D G E H W M V H Q D E K Q R K D K V F Q

GGCAATTTTG ACAATGACAC TCACAGGAAA AATGTCATCG ACCCTCCCAT CTATGCACGA 1980  
G N F D N D T H R K N V I D P P I Y A R

FIG.3C



TTCATAAGAA TCCTTCCTTG GTCCTGGTAT GGAAGGATCA CTCTGCGGTC AGAGCTGCTG 2040  
F I R I L P W S W Y G R I T L R S E L L

FspI

GGCTGCGCAG AGGAGGAATG AAGTGCGGGG CCGCACATCC CACAATGCTT TTCTTTATTT 2100  
G C A E E E

TCCTATAAGT ATCTCCACGA AATGAACTGT GTGAAGCTGA TGGAAACTGC ATTTGTTTTT 2160

HindIII

TTCAAAGTGT TCAAATTATG GTAGGCTACT GACTGTCTTT TTAGGAGTTC TAAGCTTGCC 2220

TTTTTAATAA TTTAATTGG TTTCCTTTGC TCAACTCTCT TATGTAATAT CACACTGTCT 2280

EorI

GTGAGTTACT CTTCCTGTTC TCT

2303

FIG.3D



		9		18		27		36		45		54						
5'	TCT	CTT	TAG	TCA	CCA	CTC	TCG	CCC	TCT	CCA	AGA	ATT	TGT	TTA	ACA	AAG	GCG	TGA
	S	L	*	S	P	L	S	P	S	P	R	I	C	L	T	K	R	*
			63			72			81			90			99			108
	GGA	AAG	AGA	ACG	TCT	TCT	TGA	ATT	CTT	TAG	TAG	GGG	CGG	AGT	CTG	CTG	CTG	CCC
	G	K	R	T	S	S	*	I	L	*	*	G	R	S	L	L	L	P
			117			126			135			144			153			162
	TGC	GCT	GCC	ACC	TCG	GCT	ACA	CTG	CCC	TCC	GCG	ACG	ACC	CCT	GAC	CAG	CCG	GGG
	C	A	A	T	S	A	T	L	P	S	A	T	T	P	D	Q	P	G
			171			180			189			198			207			216
	TCA	CGT	CCG	GGA	GAC	GGG	ATC	ATG	AAG	CGC	TCG	GTA	GCC	GTC	TGG	CTC	TTG	GTC
	S	R	P	G	D	G	I	M	K	R	S	V	A	V	W	L	L	V
			225			234			243			252			261			270
	GGG	CTC	AGC	CTC	GGT	GTC	CCC	CAG	TTC	GGC	AAA	GGT	GAT	ATT	TGT	GAT	CCC	AAT
	G	L	S	L	G	V	P	Q	F	G	K	G	D	I	C	D	P	N
			279			288			297			306			315			324
	CCA	TGT	GAA	AAT	GGA	GGT	ATC	TGT	TTG	CCA	GGA	TTG	GCT	GTA	GGT	TCC	TTT	TCC
	P	C	E	N	G	G	I	C	L	P	G	L	A	V	G	S	F	S
			333			342			351			360			369			378
	TGT	GAG	TGT	CCA	GAT	GGC	TTC	ACA	GAC	CCC	AAC	TGT	TCT	AGT	GTT	GTG	GAG	GTT
	C	E	C	P	D	G	F	T	D	P	N	C	S	S	V	V	E	V
			387			396			405			414			423			432
	GCA	TCA	GAT	GAA	GAA	GAA	CCA	ACT	TCA	GCA	GGT	CCC	TGC	ACT	CCT	AAT	CCA	TGC
	A	S	D	E	E	E	P	T	S	A	G	P	C	T	P	N	P	C
			441			450			459			468			477			486
	CAT	AAT	GGA	GGA	ACC	TGT	GAA	ATA	AGT	GAA	GCA	TAC	CGA	GGG	GAT	ACA	TTC	ATA
	H	N	G	G	T	C	E	I	S	E	A	Y	R	G	D	T	F	I
			495			504			513			522			531			540
	GGC	TAT	GTT	TGT	AAA	TGT	CCC	CGA	GGA	TTT	AAT	GGG	ATT	CAC	TGT	CAG	CAC	AAC
	G	Y	V	C	K	C	P	R	G	F	N	G	I	H	C	Q	H	N
			549			558			567			576			585			594
	ATA	AAT	GAA	TGC	GAA	GTT	GAG	CCT	TGC	AAA	AAT	GGT	GGA	ATA	TGT	ACA	GAT	CTT
	I	N	E	C	E	V	E	P	C	K	N	G	G	I	C	T	D	L
			603			612			621			630			639			648
	GTT	GCT	AAC	TAT	TCC	TGT	GAG	TGC	CCA	GGC	GAA	TTT	ATG	GGA	AGA	AAT	TGT	CAA
	V	A	N	Y	S	C	E	C	P	G	E	F	M	G	R	N	C	Q

FIG. 4A





		657			666			675			684			693			702
TAC	AAA	TGC	TCA	GGC	CCA	CTG	GGA	ATT	GAA	GGT	GGA	ATT	ATA	TCA	AAC	CAG	CAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	K	C	S	G	P	L	G	I	E	G	G	I	I	S	N	Q	Q
		711			720			729			738			747			756
ATC	ACA	GCT	TCC	TCT	ACT	CAC	CGA	GCT	CTT	TTT	GGA	CTC	CAA	AAA	TGG	TAT	CCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
I	T	A	S	S	T	H	R	A	L	F	G	L	Q	K	W	Y	P
		765			774			783			792			801			810
TAC	TAT	GCA	CGT	CTT	AAT	AAG	AAG	GGG	CTT	ATA	AAT	GCG	TGG	ACA	GCT	GCA	GAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	Y	A	R	L	N	K	K	G	L	I	N	A	W	T	A	A	E
		819			828			837			846			855			864
AAT	GAC	AGA	TGG	AAC	CGG	TGG	ATT	CAG	ATA	AAT	TTG	CAA	AGA	AAA	ATG	AGA	GTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
N	D	R	W	N	R	W	I	Q	I	N	L	Q	R	K	M	R	V
		873			882			891			900			909			918
ACT	GGT	GTG	ATT	ACC	CAA	GGG	GCC	AAG	AGG	ATT	GGA	AGC	CCA	GAG	TAT	ATA	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	G	V	I	T	Q	G	A	K	R	I	G	S	P	E	Y	I	K
		927			936			945			954			963			972
TTC	TAC	AAA	ATT	GCC	TAC	AGT	AAT	GAT	GGA	AAG	ACT	TGG	GCA	ATG	TAC	AAA	GTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	Y	K	I	A	Y	S	N	D	G	K	T	W	A	M	Y	K	V
		981			990			999			1008			1017			1026
AAA	GGC	ACC	AAT	GAA	GAC	ATG	GTG	TTT	CGT	GGA	AAC	ATT	GAT	AAC	AAC	ACT	CCA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
K	G	T	N	E	D	M	V	F	R	G	N	I	D	N	N	T	P
		1035			1044			1053			1062			1071			1080
TAT	GCT	AAC	TCT	TTC	ACA	CCC	CCC	ATA	AAA	GCT	CAG	TAT	GTA	AGA	CTC	TAT	CCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Y	A	N	S	F	T	P	P	I	K	A	Q	Y	V	R	L	Y	P
		1089			1098			1107			1116			1125			1134
CAA	GTT	TGT	CGA	AGA	CAT	TGC	ACT	TTG	CGA	ATG	GAA	CTT	CTT	GGC	TGT	GAA	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Q	V	C	R	R	H	C	T	L	R	M	E	L	L	G	C	E	L
		1143			1152			1161			1170			1179			1188
TCG	GGT	TGT	TCT	GAG	CCT	CTG	GGT	ATG	AAA	TCA	GGA	CAT	ATA	CAA	GAC	TAT	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	G	C	S	E	P	L	G	M	K	S	G	H	I	Q	D	Y	Q
		1197			1206			1215			1224			1233			1242
ATC	ACT	GCC	TCC	AGC	ATC	TTC	AGA	ACG	CTC	AAC	ATG	GAC	ATG	TTC	ACT	TGG	GAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
I	T	A	S	S	I	F	R	T	L	N	M	D	M	F	T	W	E
		1251			1260			1269			1278			1287			1296
CCA	AGG	AAA	GCT	CGG	CTG	GAC	AAG	CAA	GGC	AAA	GTG	AAT	GCC	TGG	ACC	TCT	GGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	R	K	A	R	L	D	K	Q	G	K	V	N	A	W	T	S	G

FIG. 4B



1305	1314	1323	1332	1341	1350
CAC AAT GAC	CAG TCA CAA	TGG TTA CAG	GTG GAT CTT	CTT GTT CCA	ACC AAA GTG
H N D	Q S Q	W L Q	V D L	L V P	T K V
1359	1368	1377	1386	1395	1404
ACT GGC ATC	ATT ACA CAA	GGA GCT AAA	GAT TTT GGT	CAT GTA CAG	TTT GTT GGC
T G I	I T Q	G A K	D F G	H V Q	F V G
1413	1422	1431	1440	1449	1458
TCC TAC AAA	CTG GCT TAC	AGC AAT GAT	GGA GAA CAC	TGG ACT GTA	TAC CAG GAT
S Y K	L A Y	S N D	G E H	W T V	Y Q D
1467	1476	1485	1494	1503	1512
GAA AAG CAA	AGA AAA GAT	AAG GTT TTC	CAG GGA AAT	TTT GAC AAT	GAC ACT CAC
E K Q	R K D	K V F	Q G N	F D N	D T H
1521	1530	1539	1548	1557	1566
AGA AAA AAT	GTC ATC GAC	CCT CCC ATC	TAT GCA CGA	CAC ATA AGA	ATC CTT CCT
R K N	V I D	P P I	Y A R	H I R	I L P
1575	1584	1593	1602	1611	1620
TGG TCC TGG	TAC GGG AGG	ATC ACA TTG	GCG TCA GAG	CTG CTG GGC	TGC ACA GAG
W S W	Y G R	I T L	A S E	L L G	C T E
1629	1638	1647	1656	1665	1674
GAG GAA TGA	GGG GAG GCT	ACA TTT CAC	AAC CGT CTT	CCC TAT TTG	GGT AAA AGT
E E *	G E A	T F H	N R L	P Y L	G K S
1683	1692	1701	1710	1719	1728
ATC TCC ATG	GAA TGA ACT	GTG TAA AAT	CTG TAG GAA	ACT GAA TGG	TTT TTT TTT
I S M	E * T	V * N	L * E	T E W	F F F
1737	1746	1755	1764	1773	
TTT TCA TGA	AAA AGT GGT	CAA ATT ATG	GTA GGC AAC	TAA CGG TGT	TTT TAC C 3'
F S *	K S G	Q I M	V G N	* R C	F Y

FIG. 4C



10	20	30	40	50	60
GACAGATGGC	CATGGATTCA	GATAAATTTG	CAAAGAAAAA	TGAGAGTCAC	TGGTGTTATT
70	80	90	100	110	120
ACCCAAGGAG	CAAAAAGGAT	TGGAAGCCCA	GAGTACATAA	AATCCTACAA	AATTGCCTAC
130	140	150	160	170	180
AGCAATGACG	GGAAGACCTG	GGCAATGTAC	AAAGTAAAAG	GCACCAATGA	AGAGATGGTC
190	200	210	220	230	240
TTTCGTGGAA	ATGTTGATAA	CAACACACCA	TATGCTAATT	CTTTCACACC	CCCAATCAAA
250	260	270	280	290	300
GCTCAGTATG	TAAGACTCTA	CCCCCAAATT	TGTCGAAGGC	ATTGTACTTT	AAGAATGGAA
310	320	330	340	350	360
CTTCTTGGCT	GTGAGCTC..	.....	.....	.....	.....

FIG. 5

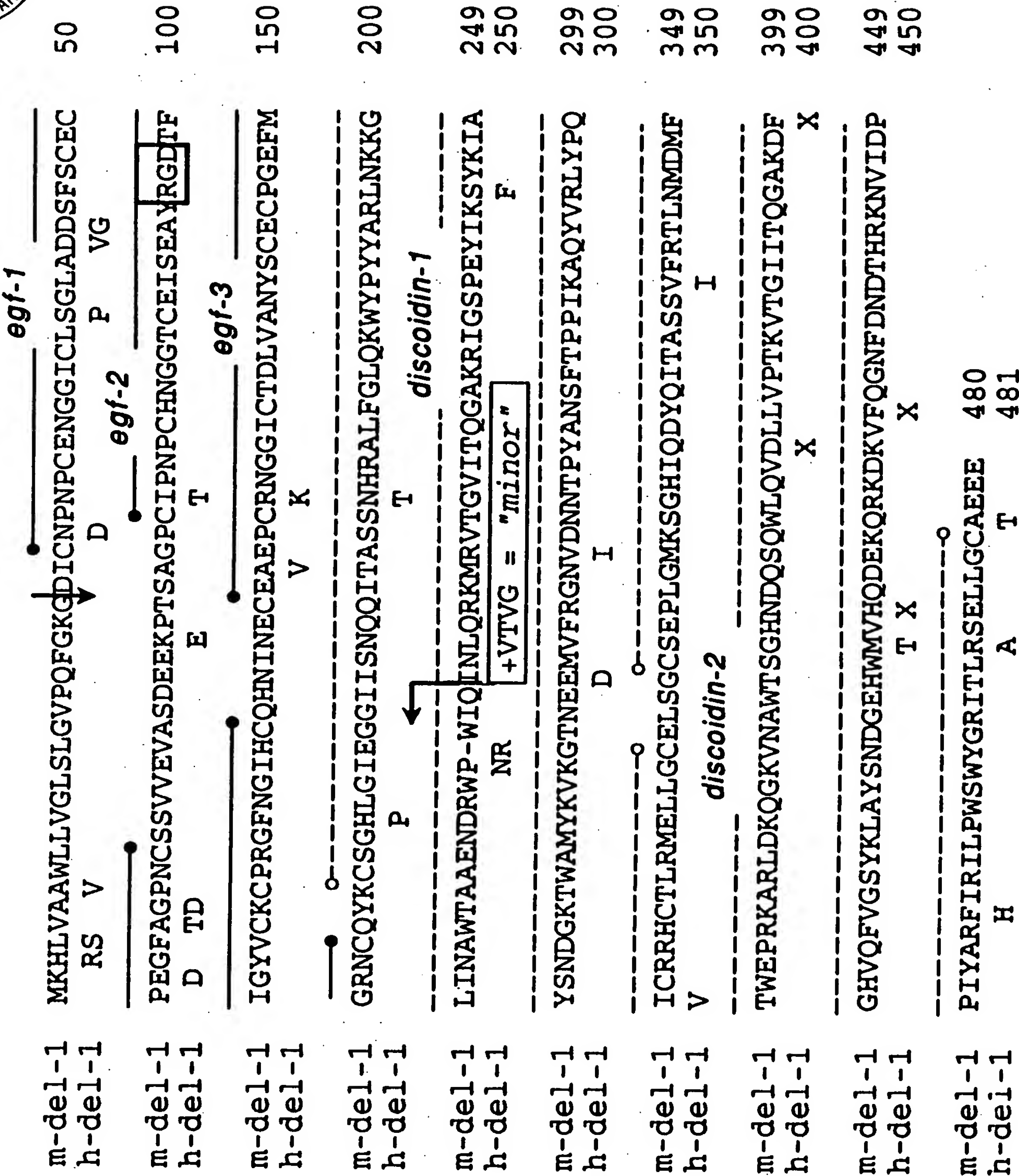


FIG.6

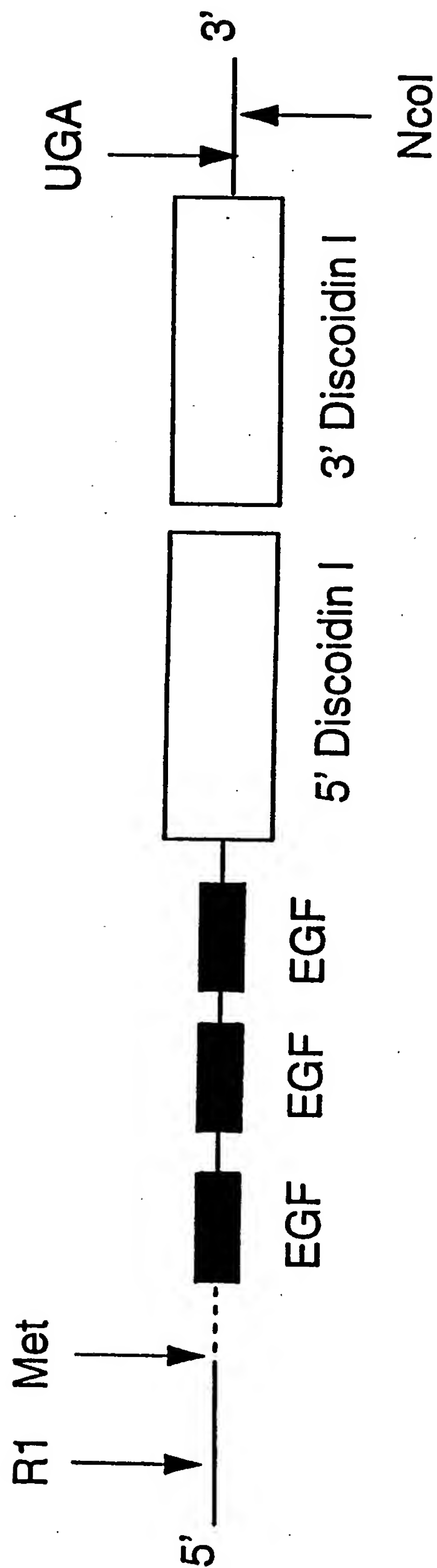
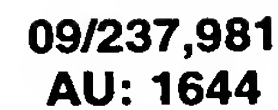


FIG. 7



**FIG. 8.**



M K R S V A V W L L V G L S L G V P O F G K G D I ...

FIG. 9

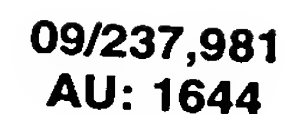
- 1) CDPNPCENGIGICLPGLAVG-----SFSCECPDGFTDPNCS SVVEVASDEEEPTSAGP
- 2) CTPNPCHNGGTCEISEAYRGDTFIGYVCKCPRGFNGIHCO HNINE
- 3) CEVEPCKNGGICTDLVA-----NYSCECPGEFMGRNCQ YK

CONSENSUS C---PC-NGG-C-----Y-C-C--GY-G--C--  
EGF DOMAIN F F

FIG. 10

	9			18			27			36			45			54		
5'	-GT	GAT	ATT	TGT	GAT	CCC	AAT	CCA	TGT	GAA	AAT	GGA	GGT	ATC	TGT	TTG	CCA	GGA
	X	D	I	C	D	P	N	P	C	E	N	G	G	I	C	L	P	G
		63				72			81			90			99			108
	TTG	GCT	GTA	GGT	TCC	TTT	TCC	TGT	GAG	TGT	CCA	GAT	GGC	TTC	ACA	GAC	CCC	AAC
	L	A	V	G	S	F	S	C	E	C	P	D	G	F	T	D	P	N
		117				126			135			144			153			162
	TGT	TCT	AGT	GTT	GTG	GAG	GTT	GGT	CCC	TGC	ACT	CCT	AAT	CCA	TGC	CAT	AAT	GGA
	C	S	S	V	V	E	V	G	P	C	T	P	N	P	C	H	N	G
		171				180			189			198			207			216
	GGA	ACC	TGT	GAA	ATA	AGT	GAA	GCA	TAC	CGA	GGG	GAT	ACA	TTC	ATA	GGC	TAT	GTT
	G	T	C	E	I	S	E	A	Y	R	G	D	T	F	I	G	Y	V
		225				234			243			252			261			270
	TGT	AAA	TGT	CCC	CGA	GGA	TTT	AAT	GGG	ATT	CAC	TGT	CAG	CAC	AAC	ATA	AAT	GAA
	C	K	C	P	R	G	F	N	G	I	H	C	Q	H	N	I	N	E
		279				288			297			306						
	TGC	GAA	GTT	GAG	CCT	TGC	AAA	AAT	GGT	GGA	ATA	TGT	ACA	G	3'			
	C	E	V	E	P	C	K	N	G	G	I	C	T					

FIG. 11



**FIG. 12A**





BspMI

AACTGCTCTA GTGTTGTGGA GGTTCATCA GATGAAGAAA AGCCTACTTC AGCAGGTCCC 780  
N C S S V V E V A S D E E K P T S A G P

TGCATCCCTA ACCCATGCCA TAACGGAGGA ACCTGTGAGA TAAGCGAAGC CTATCGAGGA 840  
C I P N P C H N G G T C E I S E A Y R G

GACACATTCA TAGGCTATGT TTGTAAATGT CCTCGGGGAT TTAATGGGAT TCACTGTCAG 900  
D T F I G Y V C K C P R G F N G I H C Q

CACAATATAA ATGAATGTGA AGCTGAGCCT TGCAGAAATG GCGGAATATG TACCGACCTT 960  
H N I N E C E A E P C R N G G I C T D L

BsmI

GTGCTAACT ACTCTTGTA ATGCCCAGGA GAATTTATGG GACGAAATTG TCAATATAAA 1020  
V A N Y S C E C P G E F M G R N C Q Y K

TGCTCTGGGC ACTTGGAAT CGAAGGTGGG ATCATATCTA ATCAGCAAAT CACAGCTTCA 1080  
C S G H L G I E G G I I S N Q Q I T A S

SacI

Ecl136II

TCTAATCACC GAGCTCTTTT TGGACTCCAG AAGTGGTATC CCTACTATGC TAGACTTAAT 1140  
S N H R A L F G L Q K W Y P Y Y A R L N

NcoI

MscI

BalI

PvuII

AAGAAGGCC TTATAAATGC CTGGACAGCT GCTGAAAATG ACAGATGGCC ATGGATTCAG 1200  
K K G L I N A W T A A E N D R W P W I Q

GTAACAGTGG GATGAGACAA ATCCATTTC CAAATTATCA GAATCATTAT AGAAGTAGGT 1260  
V T V G

TAGGGAGAAT TGGCTGTGAT TCTTTCTCAT GGTAAAATG TGATTAGTT CAGAATTAAC 1320

FIG.12B



09/237,981  
AU: 1644

ATGGTTGGAA ACTCTAAAA ATGTGGAAAA CAGGAACATT CTATGTCTGA AAATCTGAAA 1380

ATAGCATCAA GATGAAAACA TTCTTTAGTC ATAAATATAC TCTTTTAAGT TATAGTAGAG 1440

BglII

AAAAGATCT TATCATTTC TAAGTGGACT TTTGGGATAG CATTGGAAAT GTAAATGAAA 1500

SspI

TAAATACCTA ATTGAAAAA GTTTATTCTA AAGTGTAAT ATTAGCAAC AGATTCAGAG 1560

ACAAGAAAGT AACAATTCAA TCTGTGTATT TTTGTGAGA AATAGTTTCC CATGTGCAA 1620

FspI

BspHI

PstI

TATAAAGTGC GCATCATATC ATGATAATAT CCAACTGTCT GCAGAACTCC CTTTCATAAA 1680

TGAGAGAATT TTAATTCATA GTGCCTTATA TCCTCATCAG CCATCTGACT TTAACACAGA 1740

NsiI

AGAAAACAAT GAAATGATGC ATTAAGTGCT TTGCTAGAAG AAACATCATA GCAAAGCTGA 1800

HindIII

XhoI

PaeR7I

TAGCCACAT TCTGTGCANN NAAGCTTCCA GAGCACTCGA GAAAAGCAG AAATGAGATG 1860

BclI

TTTTATGAAA ACCGAAAAGA TAATCTGATT TCTGTGAAAT ATACTTTTGA TCATGTGGTT 1920

CTTTAAGATA GTCACATAACA AGTCATTAGT AGCAGATACC AAATGGGAGA AAATTTCCAG 1980

Bst1107I

TATACTGAGG GTCAAGGCAG TCATGCTGAA ACTACATGAG GTCAGGAAAG TTTTGAAATA 2040

FIG.12C



AGGTGATTTT GGAAGGATAC CTTCAACTGG CCTAGATTTT CAAGAAACAG TGTAAATCAAC 2100

AGCCAAACAT GAGAATCTAG CTAACAGCAT TTAGAAAACC AGAACTAAGA GTGTTACTGG 2160

DraI

GGAATTGCAT TTAAATCCAG TATGAGAGTT TGCAAATGCC GTATTCTTCT AAGGGGTTTG 2220

NcoI

TGCCACATTT TGTTACCATG GAGTCCTCTG TAAGAACTTT ATTAGATAAA TCATCTTTAC 2280

EcoRI

ACTATAATTT GAATAAAAGC CGGAATTC

2308

FIG.12D



09/237,981  
AU: 1644

22713 U.S. PTO  
052704

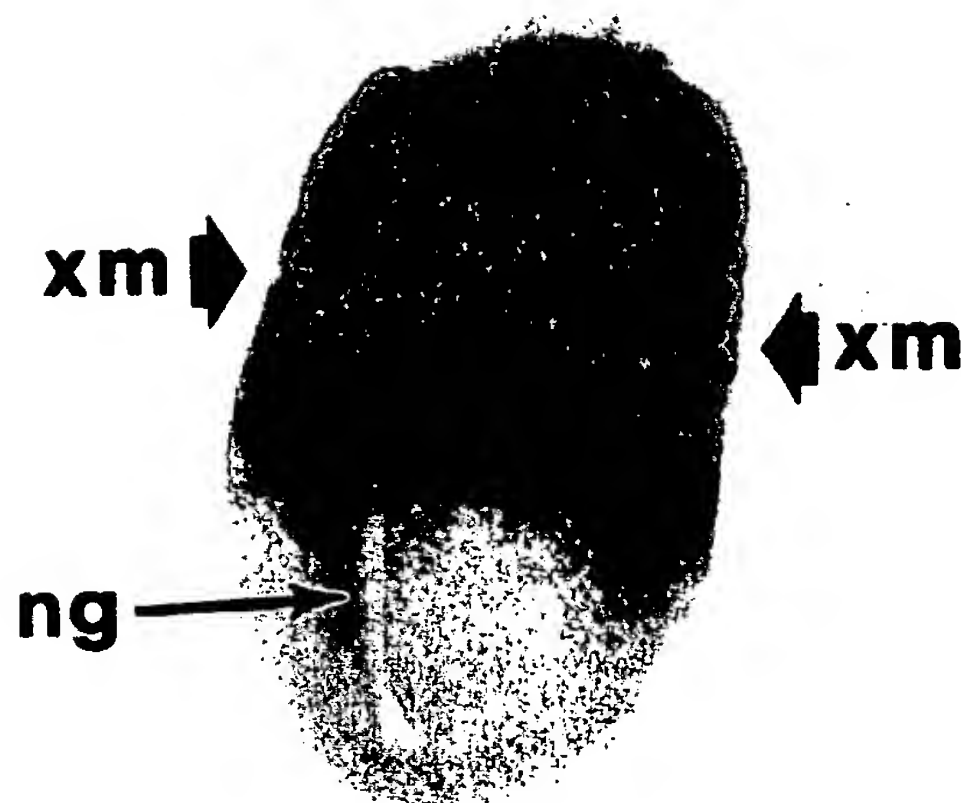


FIG.13A

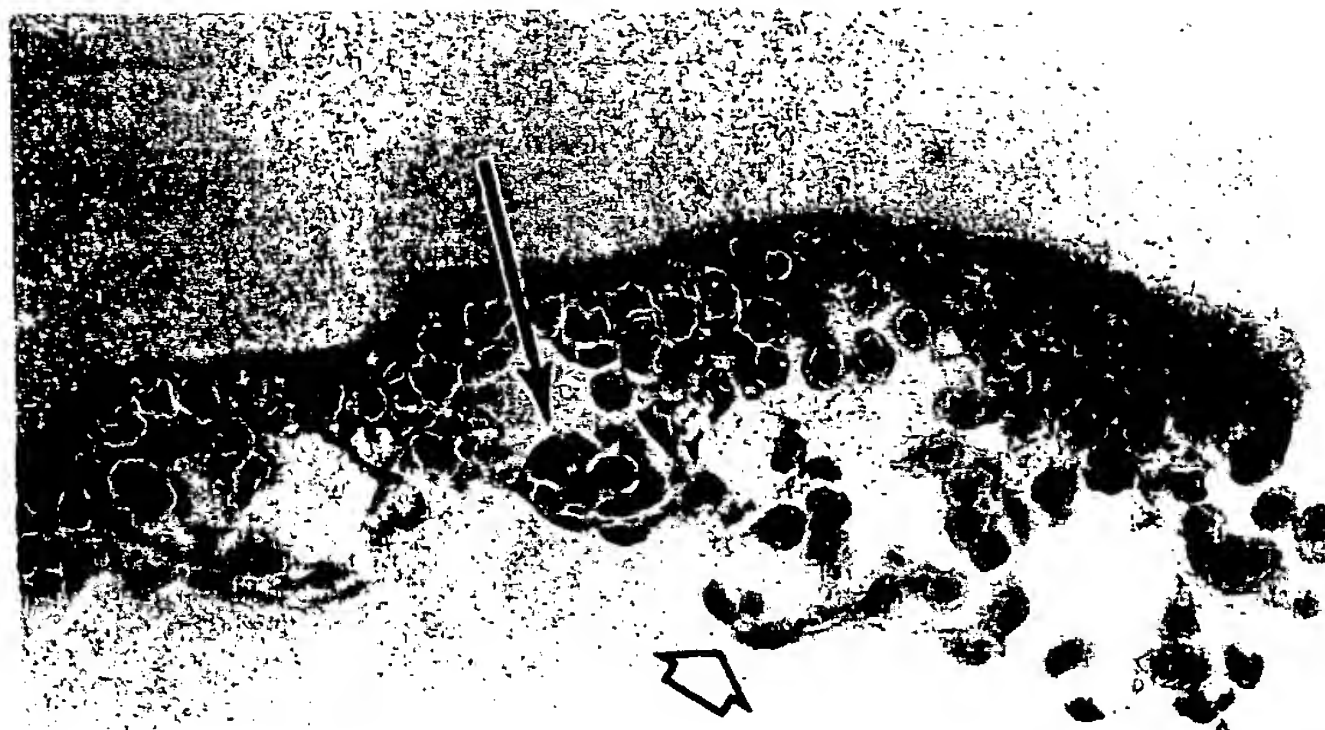


FIG.13B

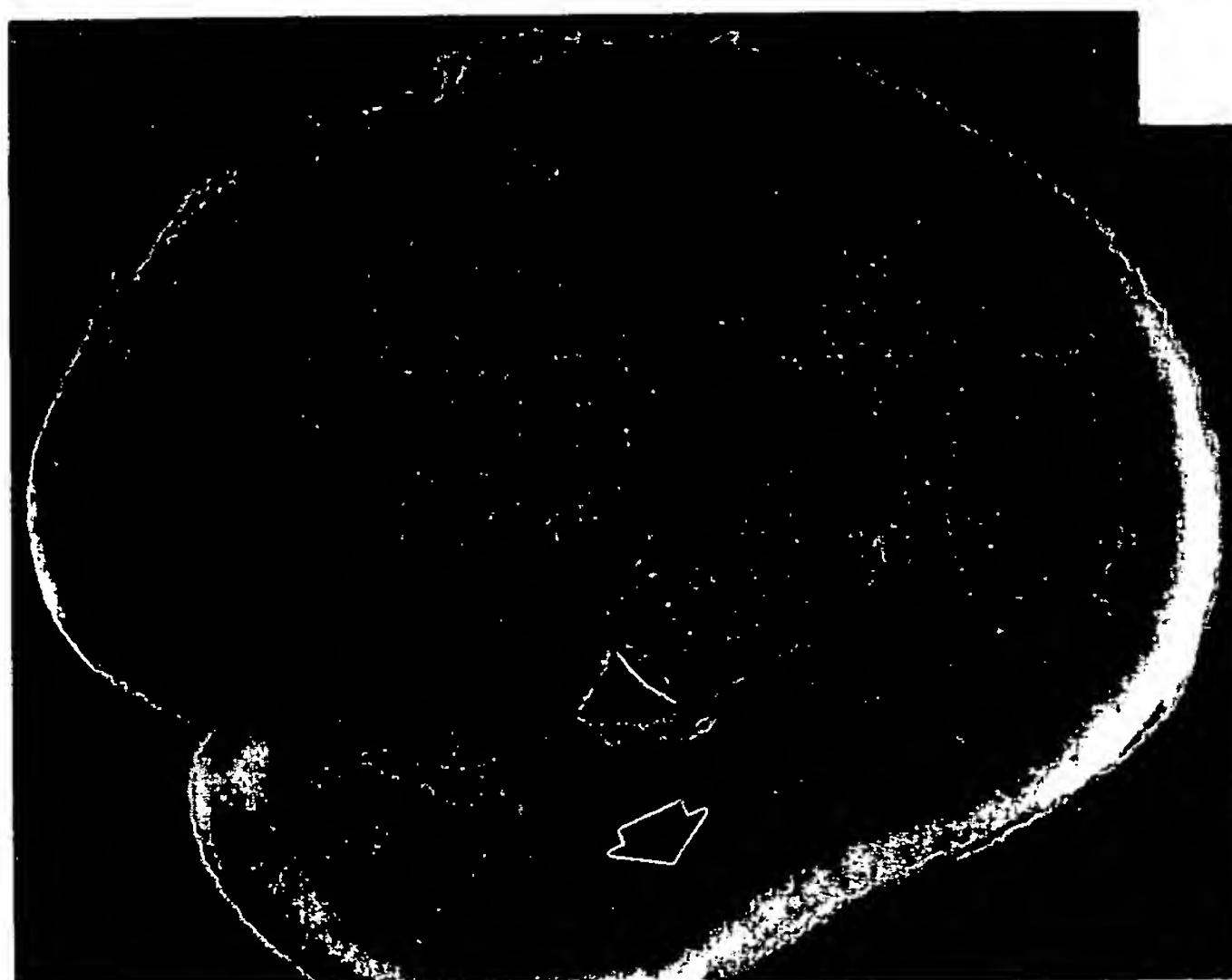


FIG. 13C

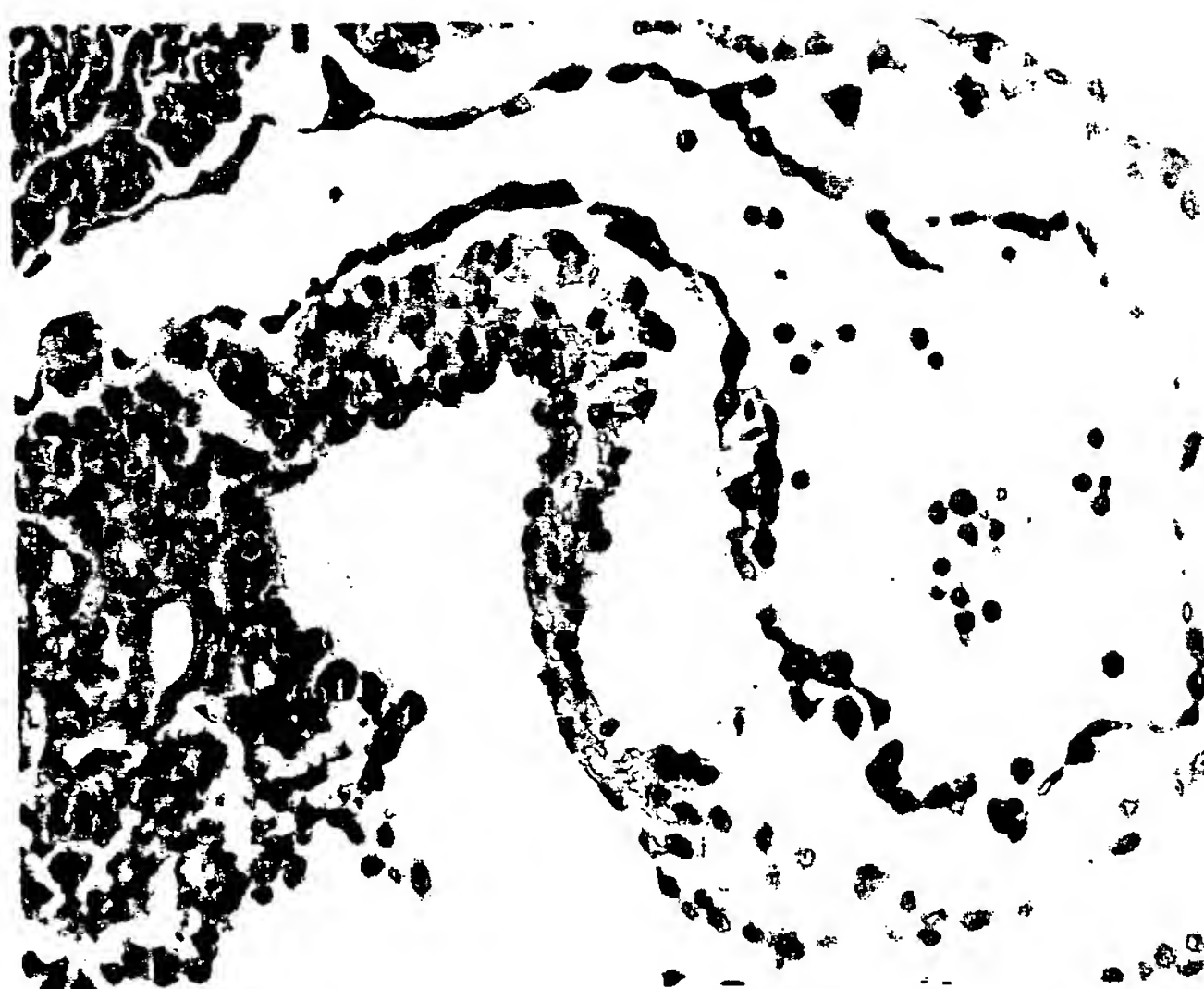


FIG. 13D

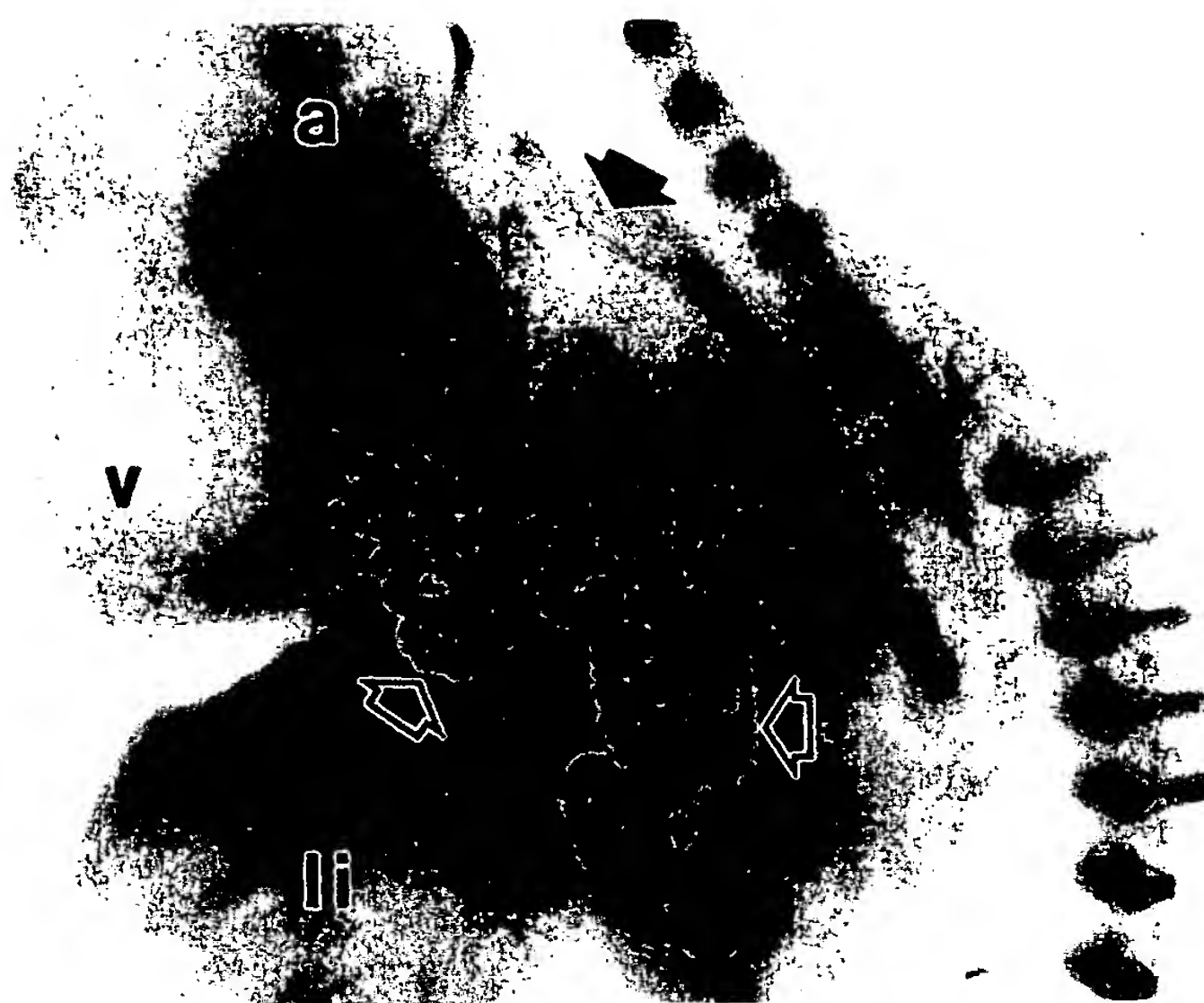


FIG. 13E

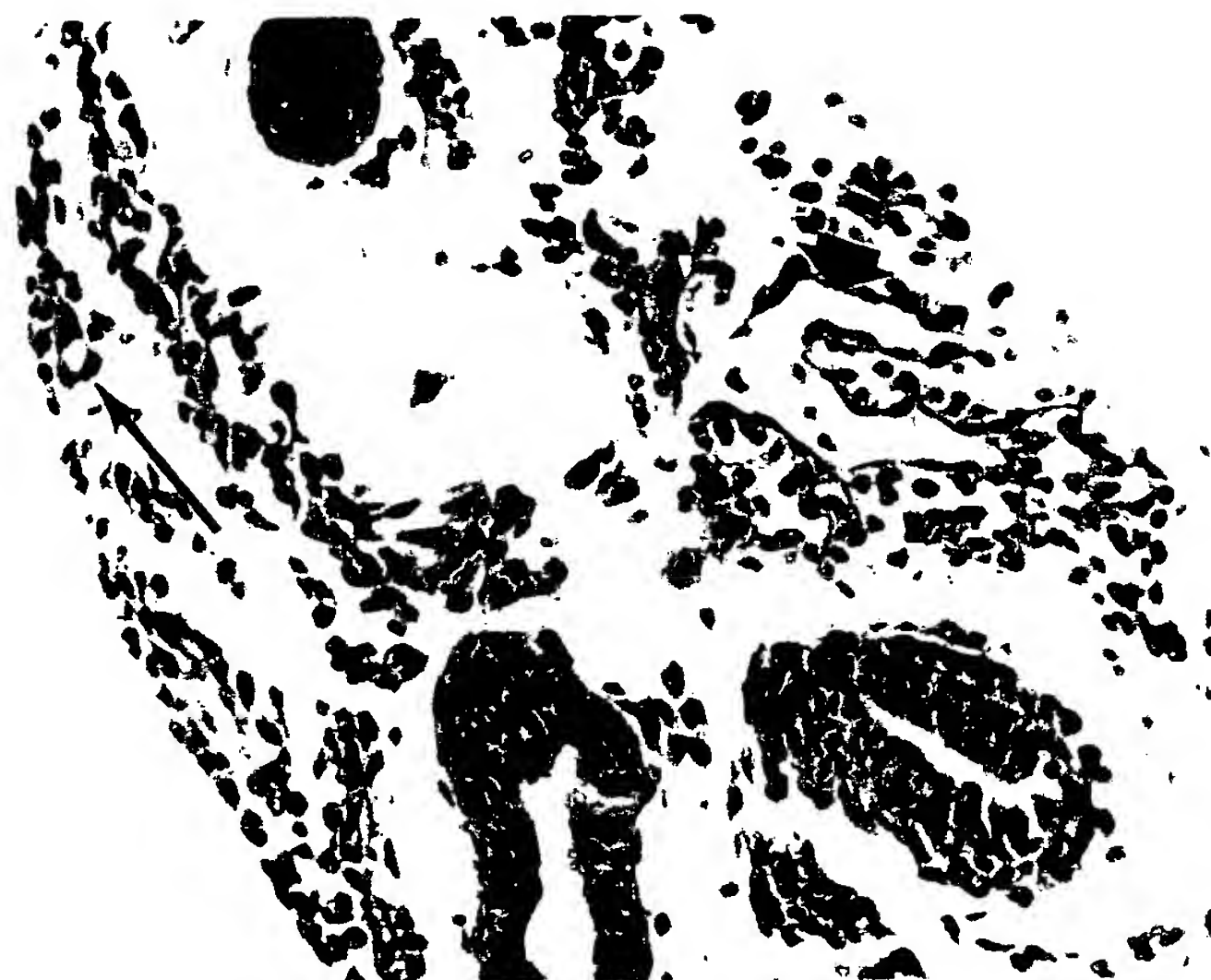


FIG. 13F





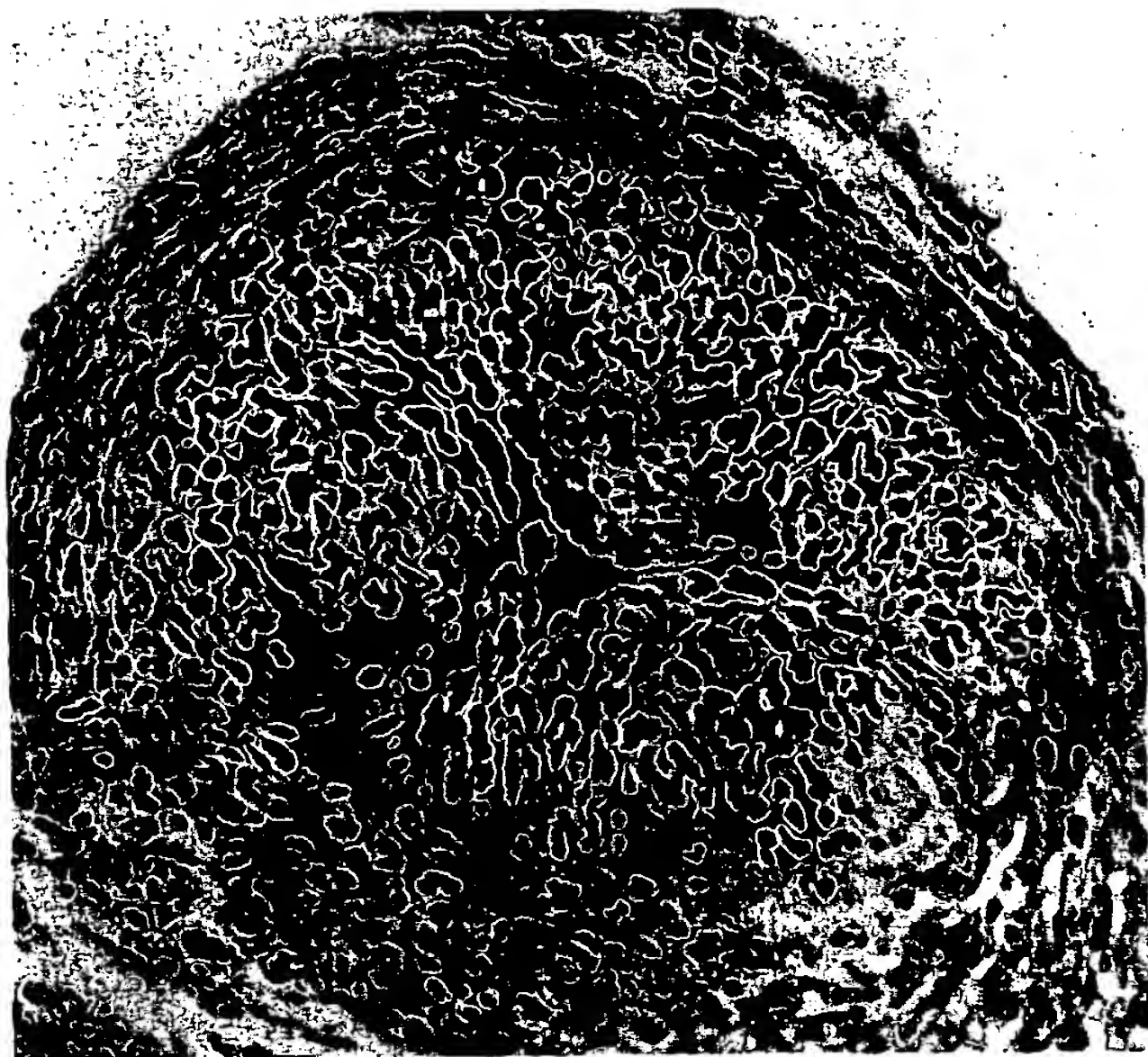


FIG.13G

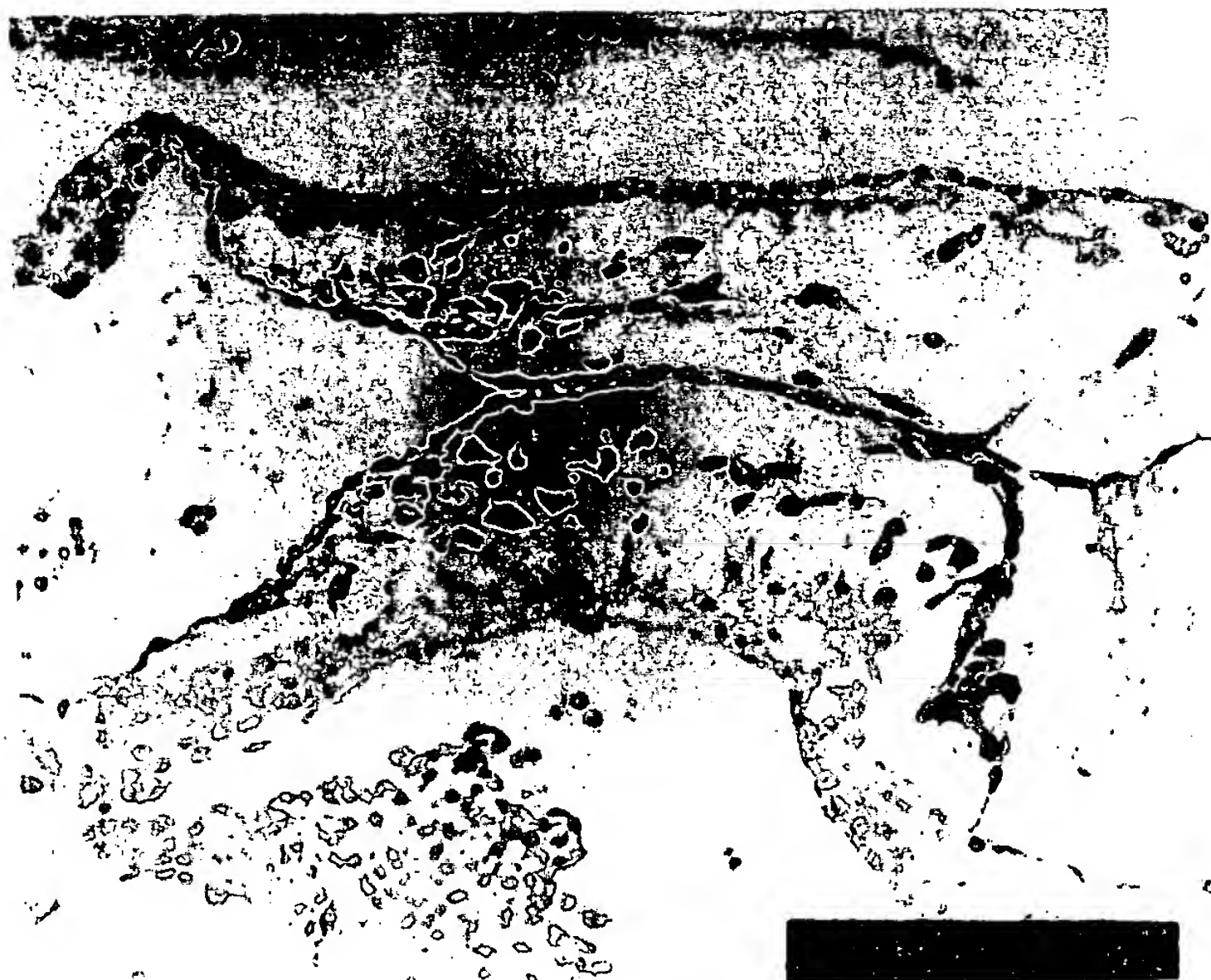


FIG.13H



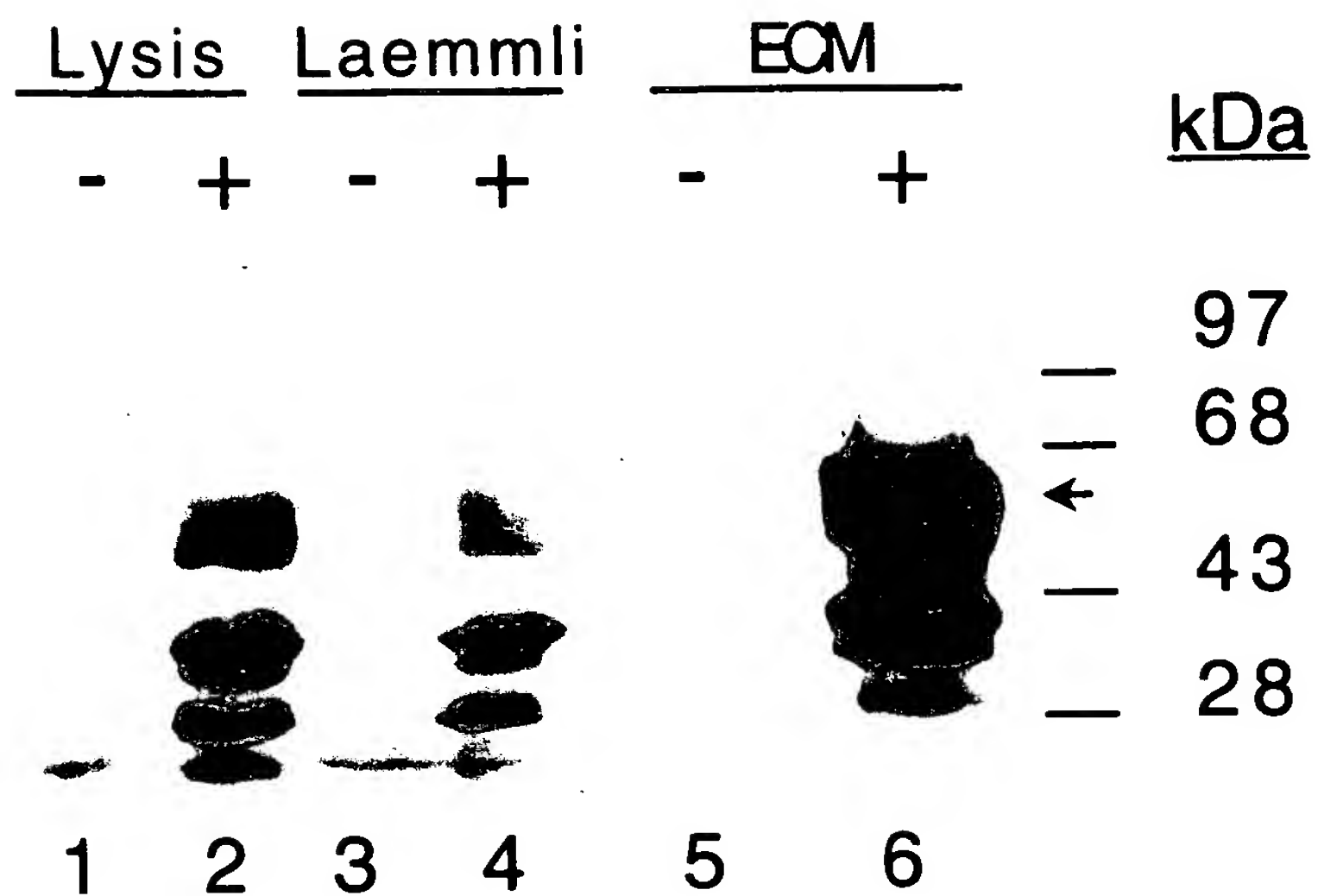


FIG.14A



FIG.14B



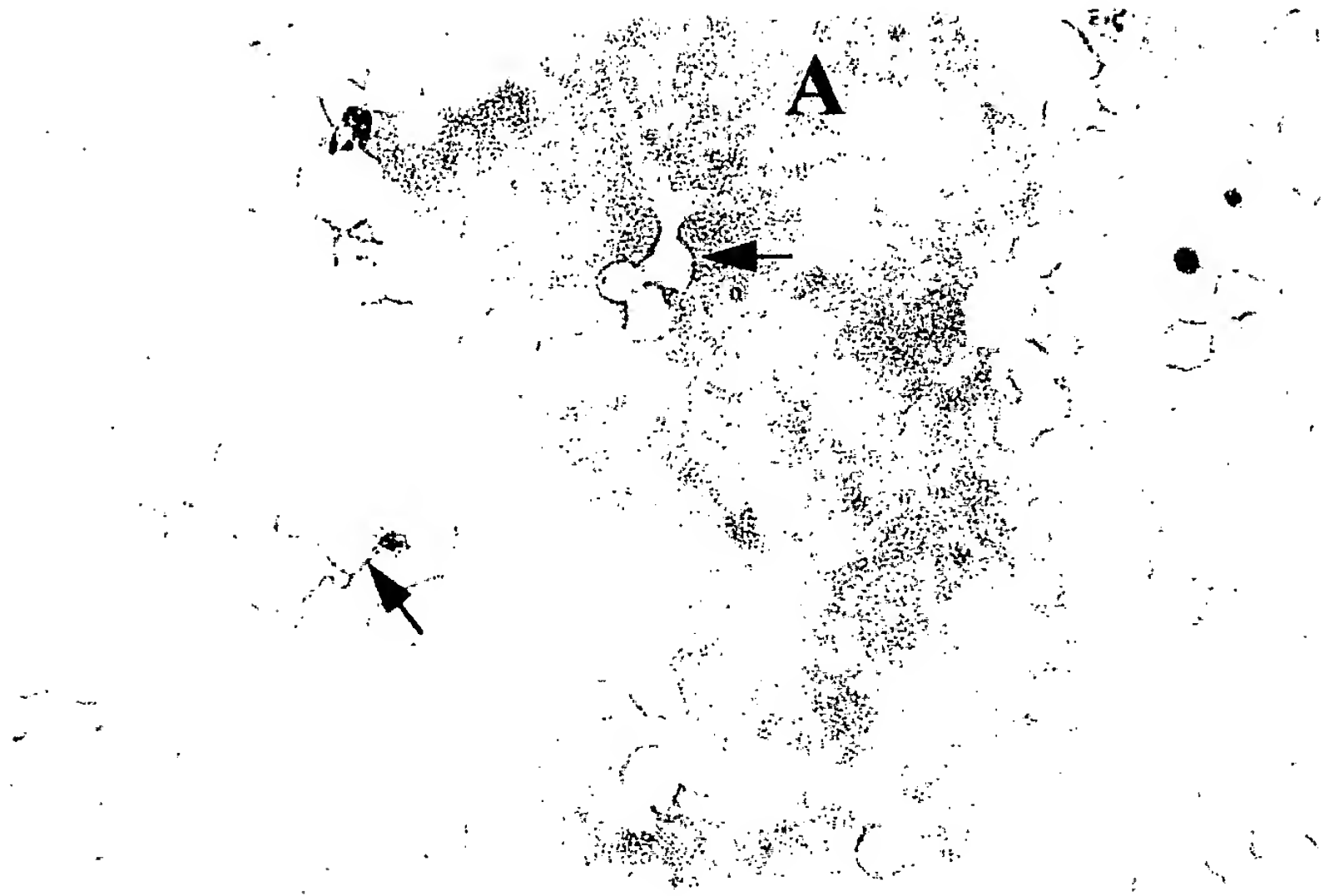


FIG.15A

FIG.15B

FIG.16



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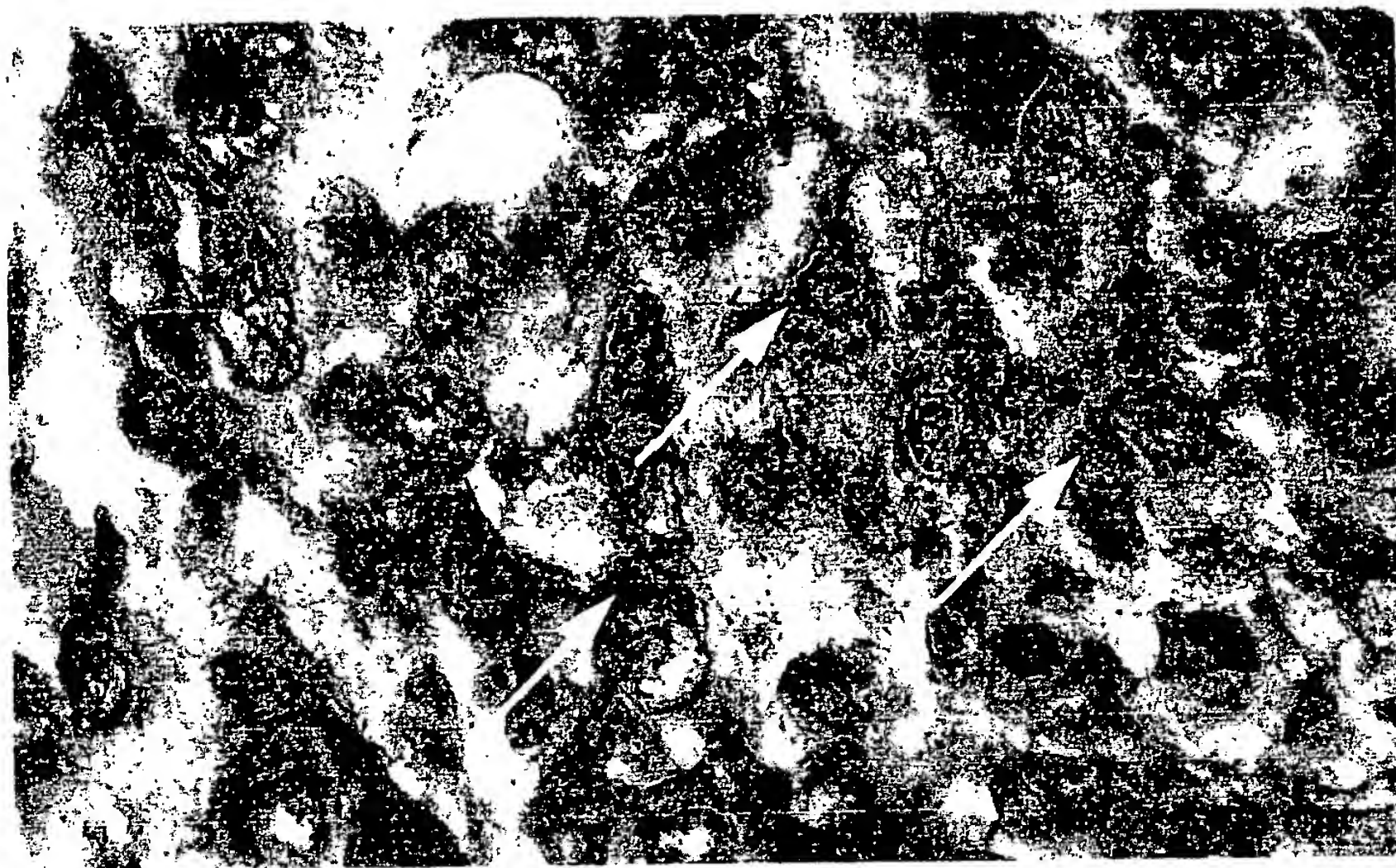


FIG.17A

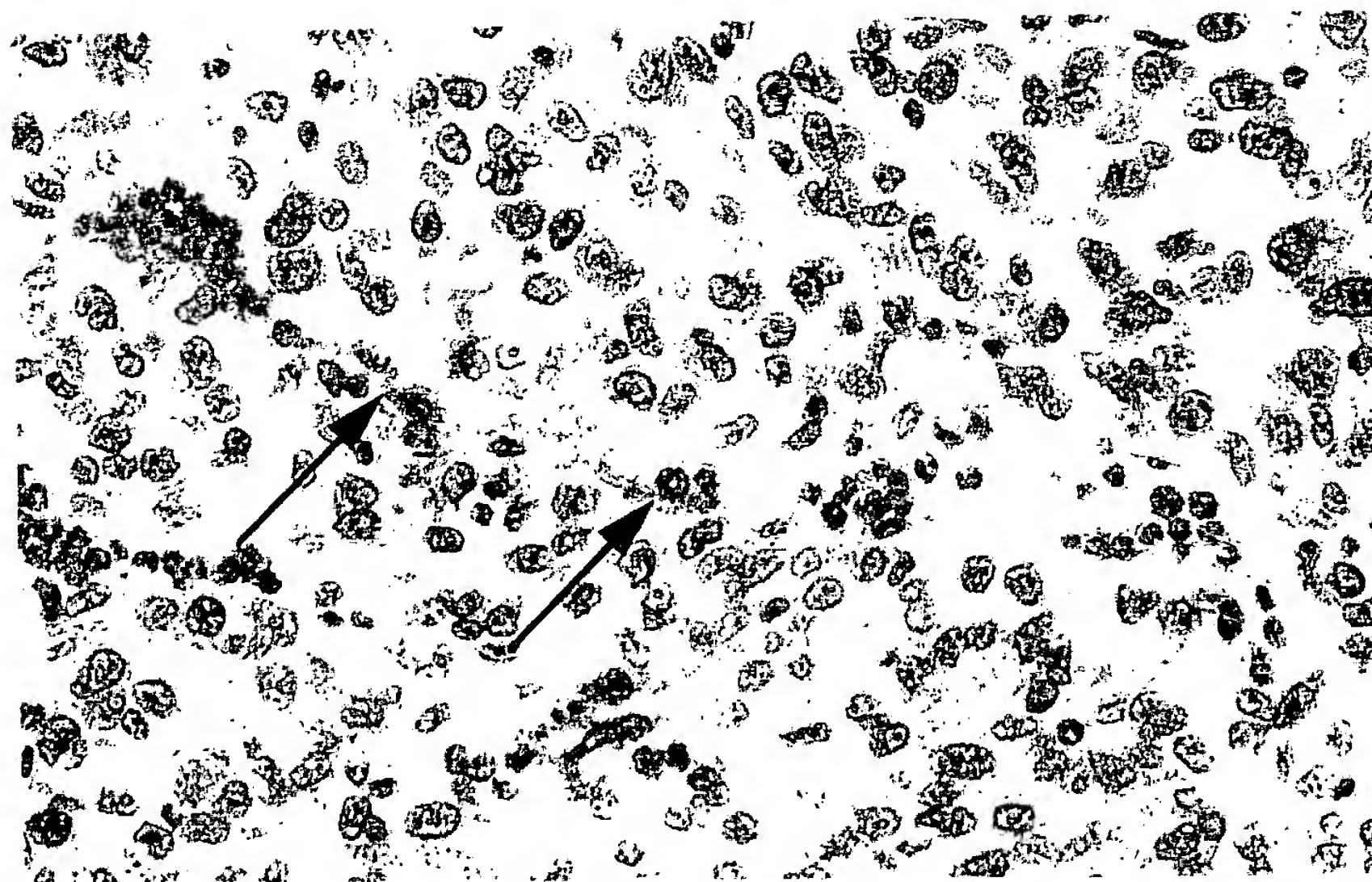


FIG.17B

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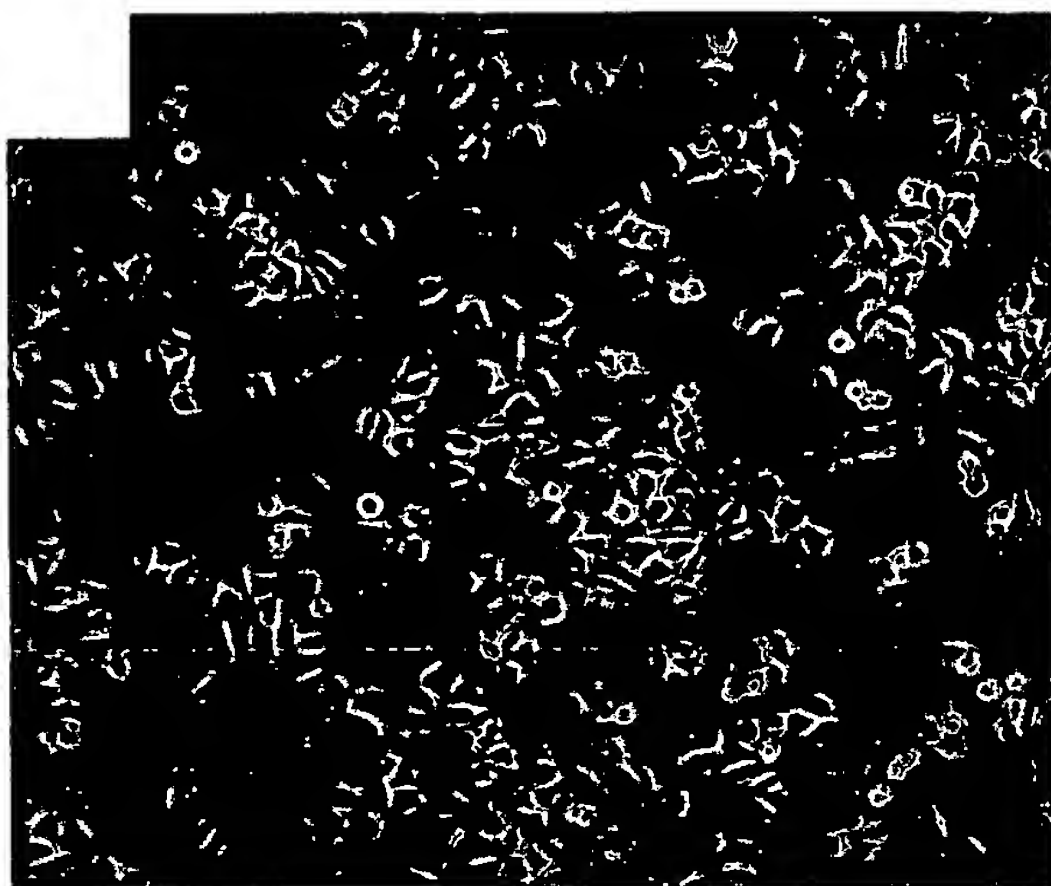


FIG.18A



FIG.18B



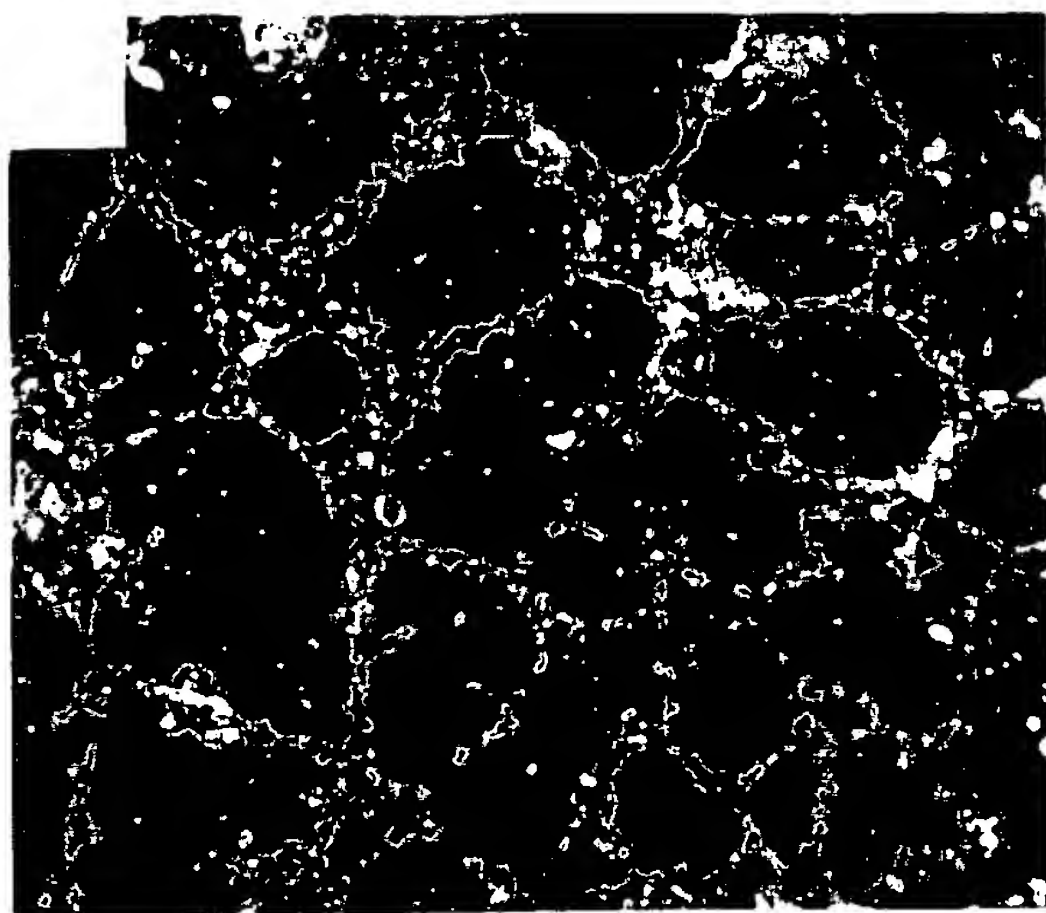


FIG. 18C

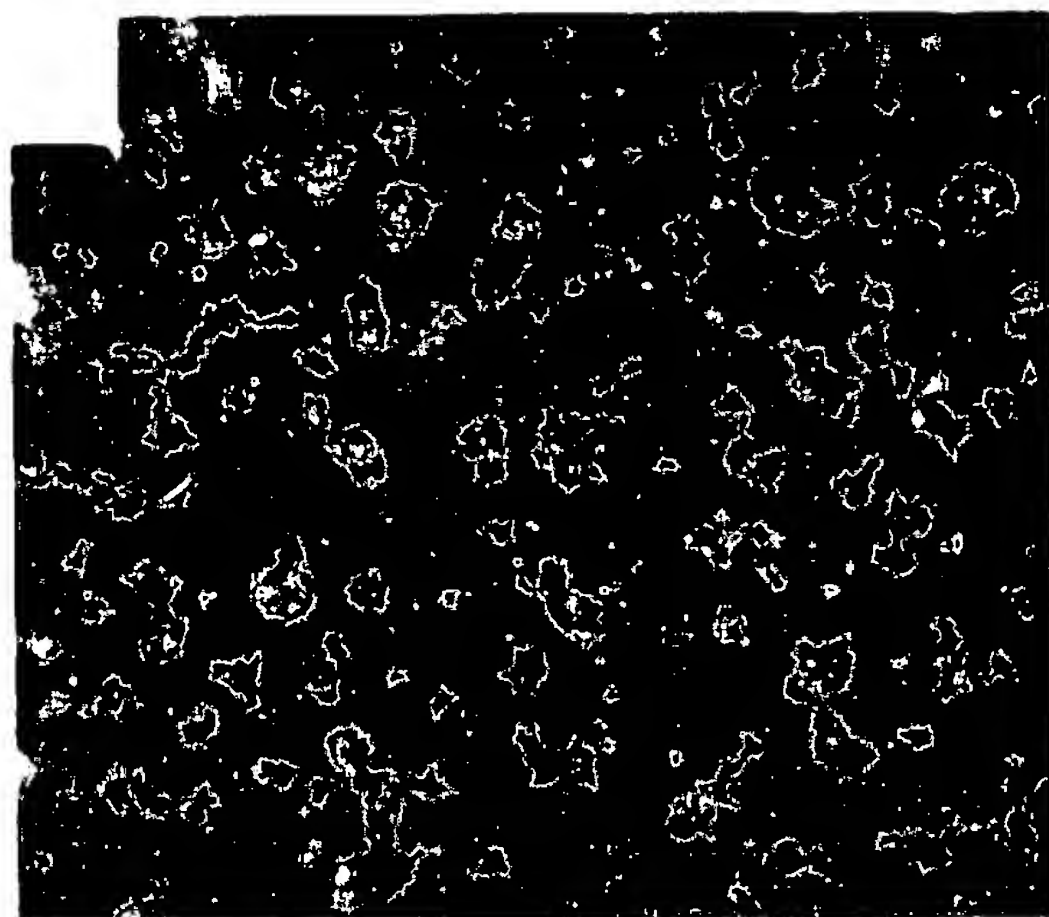


FIG. 18D

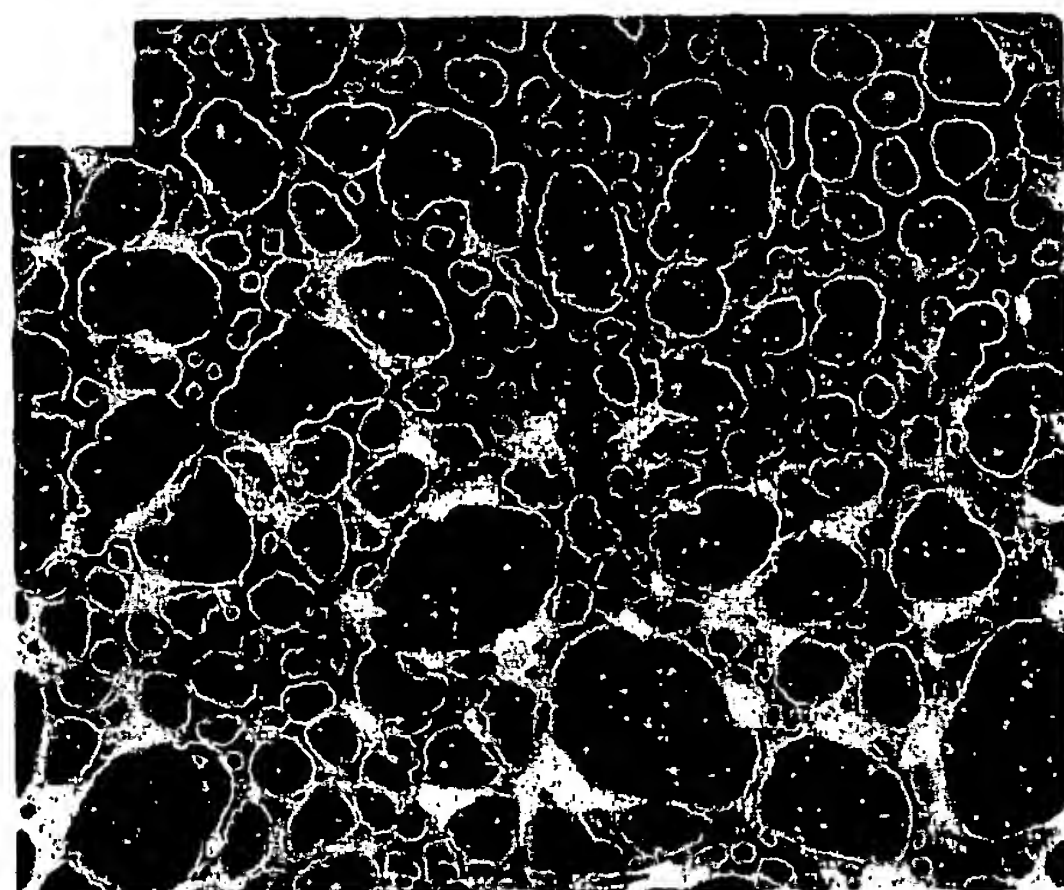


FIG.18E

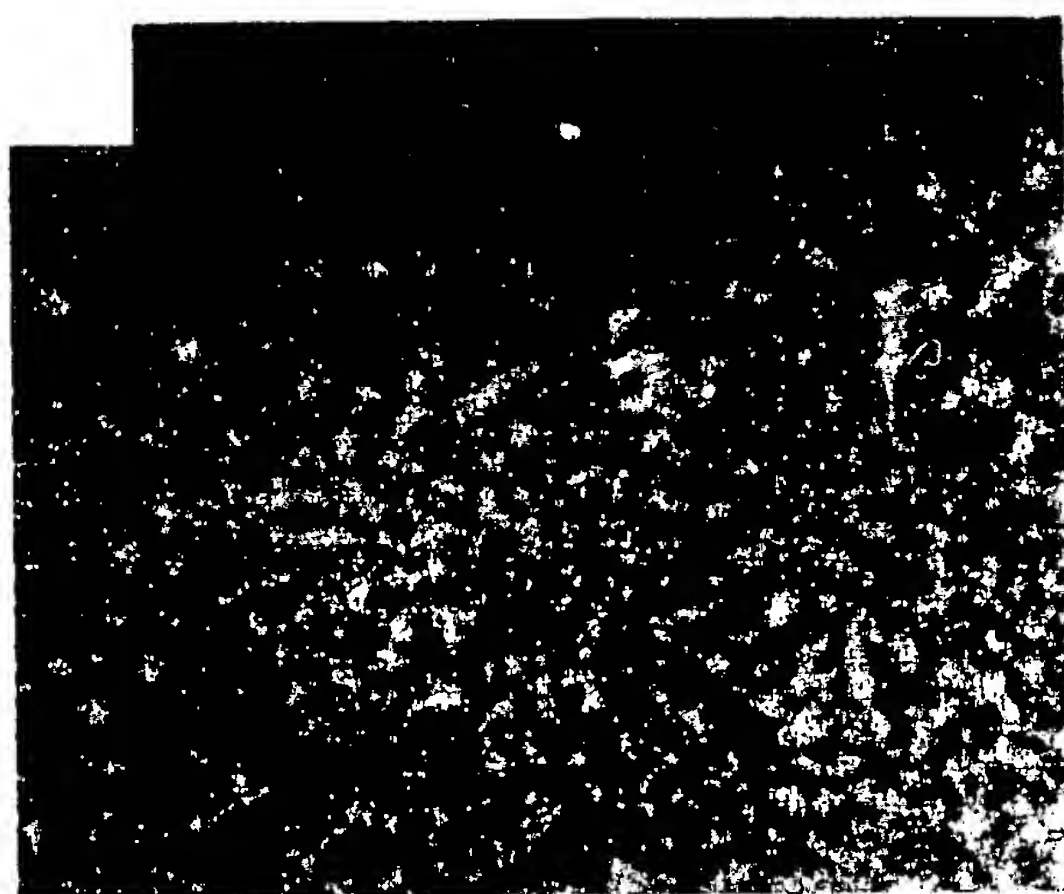


FIG.18F



22713 U.S. PTO



052704

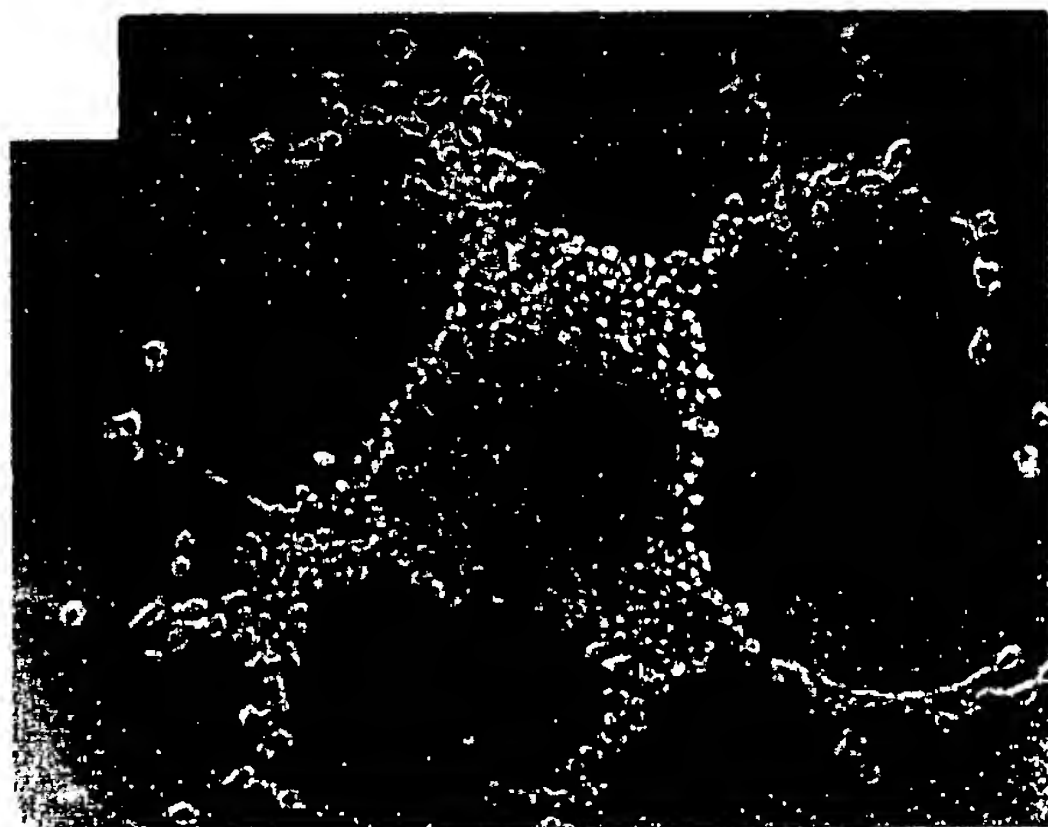


FIG. 18G

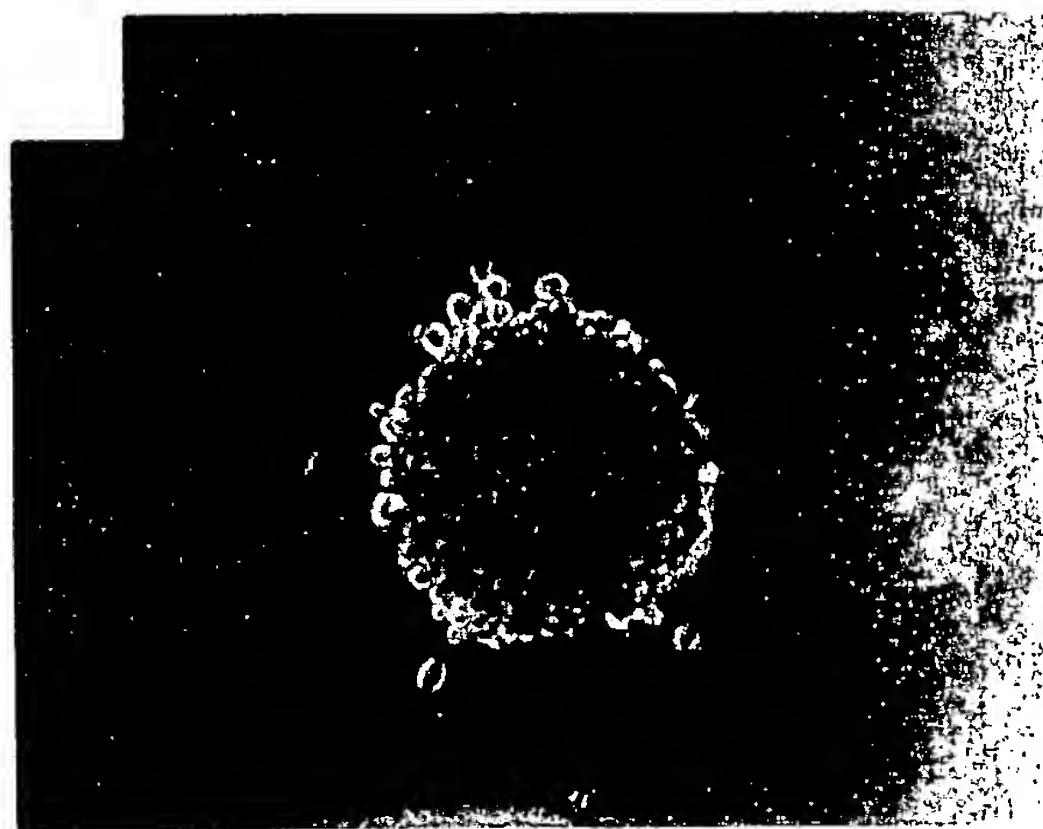


FIG. 18H

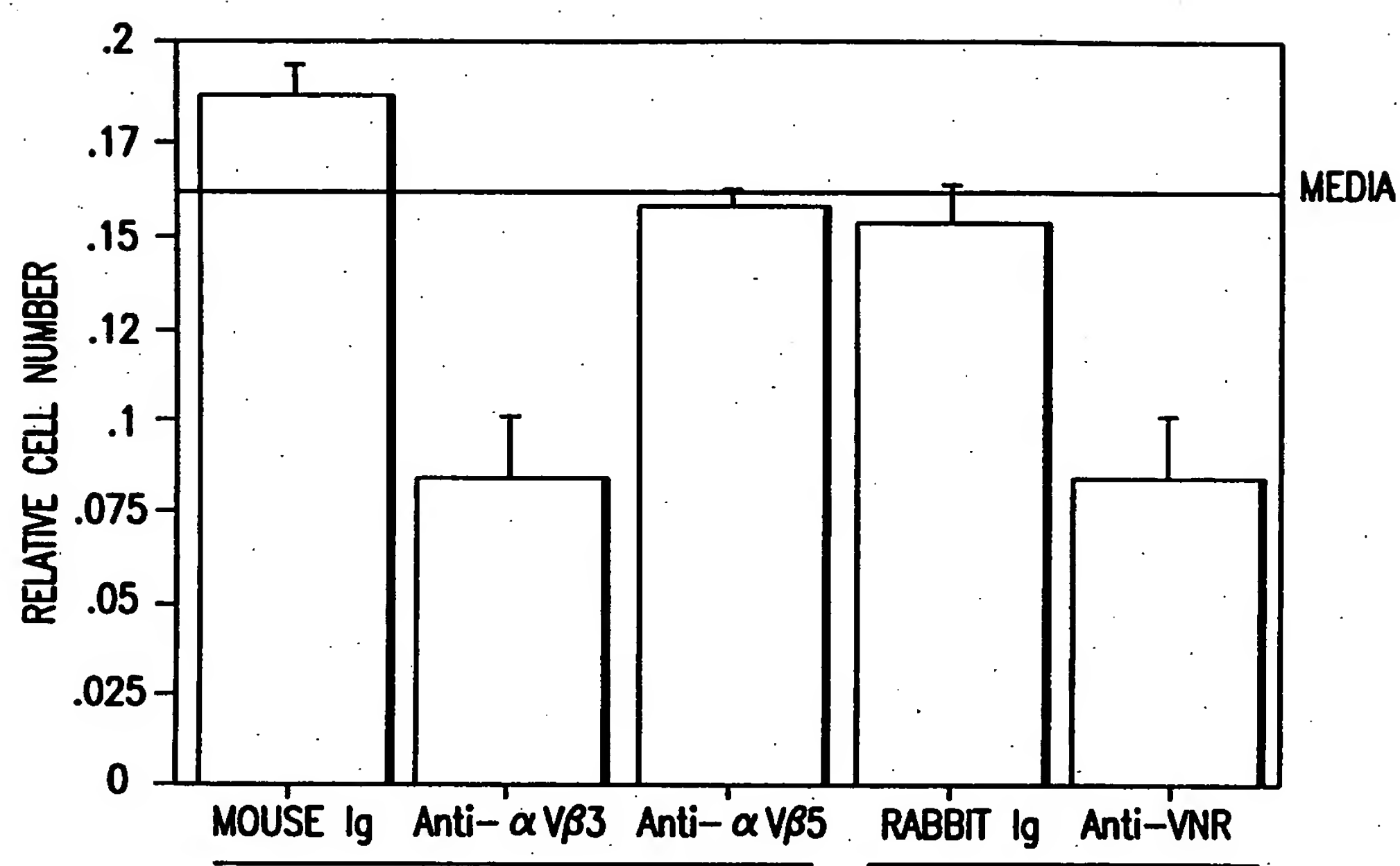


FIG.19

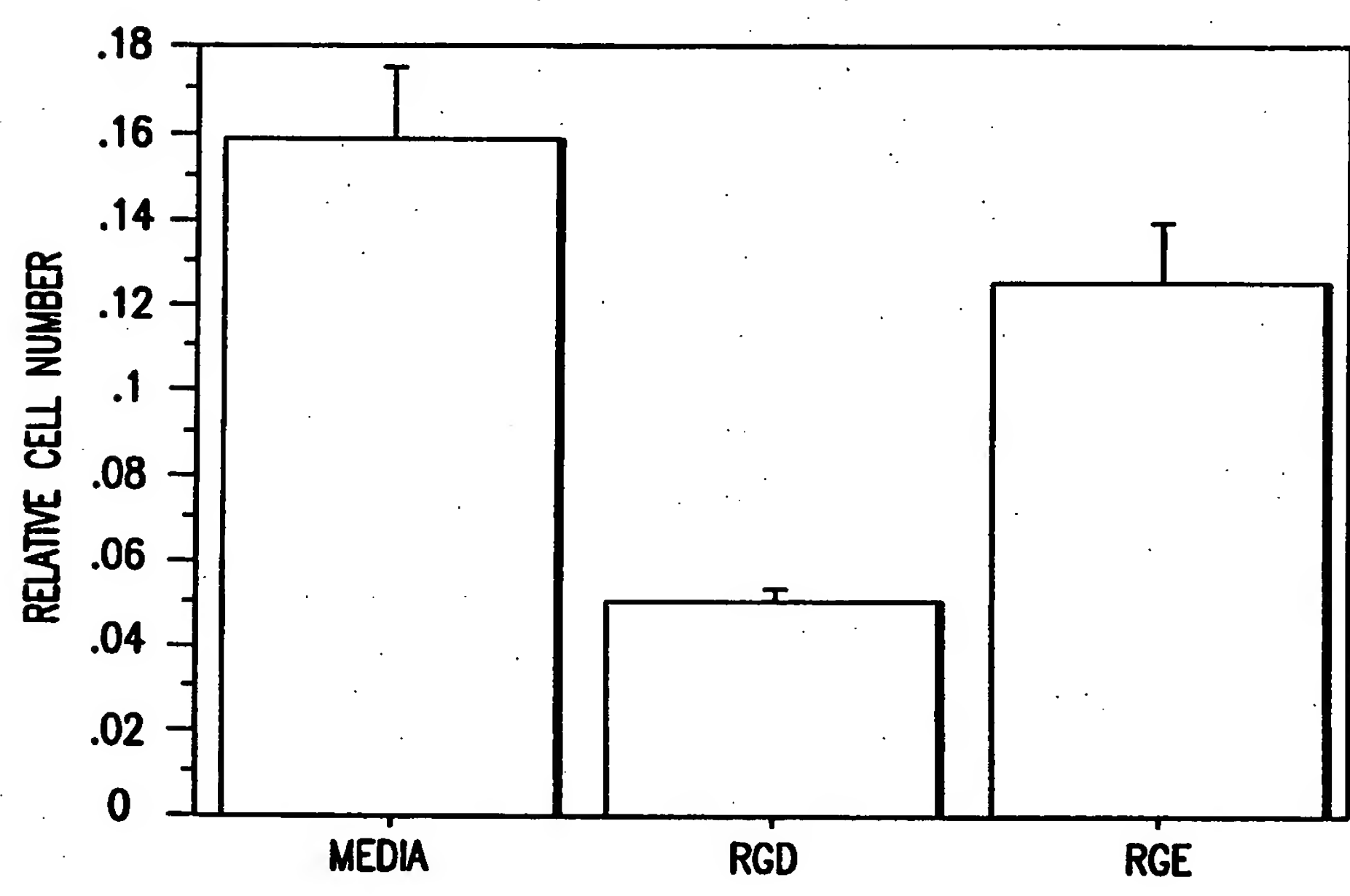


FIG.20





FIG.21A

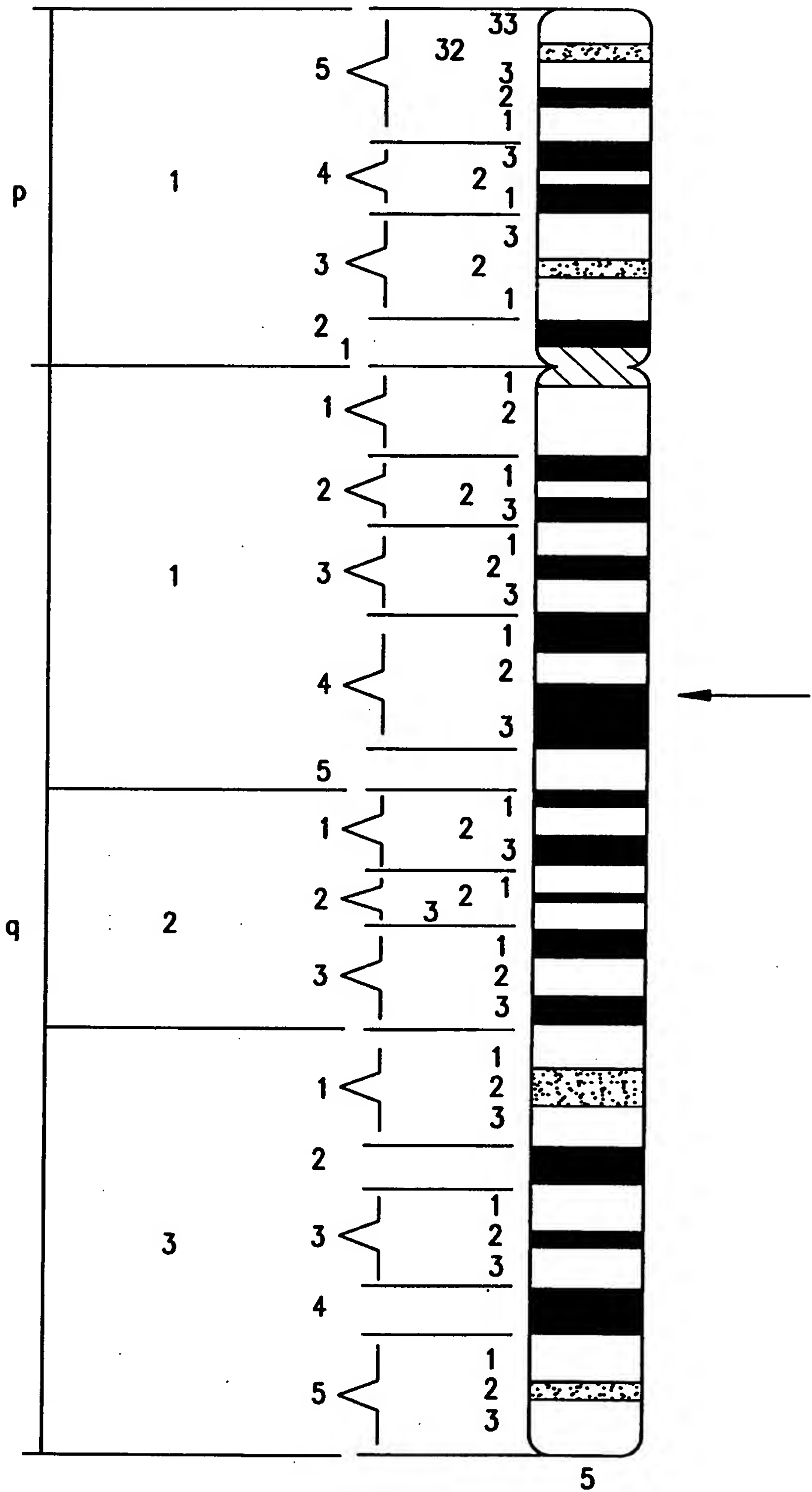


FIG. 21B